

Genome version 4.5  
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OM protein - protein search, using sw model

Run on: February 20, 2002, 16:26:19, Search time: 25.85 seconds

(without alignments)  
1231.759 million cell updates/sec

Hit(s): US-09-544-176A-13

Score(s): 2354  
Sequence: 1 MTELEMSLQGLANAVLL.....LAEKVCVKISMKRLPMN 418

Search table: HUSOM62

Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174572 residues

Total number of hits satisfying chosen parameters: 219241

Minimum hit seq length: 0  
Maximum hit seq length: 200000000

Post processing: Minimum Match: 0%

Maximum Match: 100%

Listing first 45 summaries

Database:

1: PIR-66\*  
2: PIR-67\*  
3: PIR-68\*  
4: PIR-69\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1804.5	75.7	419	2 S69207	vascular endothelial
2	211	10.2	1797	2 S69167	Ballblat, 109, 74
3	211.5	9.0	232	2 A41551	vascular endothelial
4	191.5	8.1	190	2 S62159	vascular endothelial
5	188.5	8.0	190	2 B44881	vascular endothelial
6	188.5	8.0	190	2 A5987	glioma-derived vas
7	179.5	7.6	190	2 B40080	vascular endothelial
8	174.5	7.4	214	2 A14881	vascular endothelial
9	174	7.4	190	2 S6952	18K secretory prote
10	170.5	7.2	1187	2 B18355	hypothetical prote
11	164.5	7.0	188	2 B04680	vascular endothelial
12	158.5	6.7	146	2 S6956	ovine vascular end
13	157.5	6.7	120	2 A33787	vascular endothelial
14	152	6.5	2871	2 A55624	fibroblast precu
15	150	6.4	148	2 B49530	16K vascular endot
16	144	6.1	4002	2 A47221	fibroblast precu
17	143.5	6.1	133	2 B49530	vascular endothelial
18	141.5	6.0	8712	2 S18253	laminin alpha-1 ch
19	141	6.0	149	2 A41246	placental growth f
20	141	6.0	1111	2 T36972	hypothetical prote
21	140	5.9	1077	2 A55567	probable cysteine
22	140	5.9	2971	2 A55567	fibroblast precu
23	138.5	5.9	1819	2 A42130	tenascin precursor
24	138	5.9	847	2 A42132	tenascin-like peptid
25	137.5	5.8	1104	2 A18869	transcription fact
26	137.5	5.8	1203	2 A49175	transcription fact
27	137.5	5.8	1664	2 B39079	transcription fact
28	137	5.7	207	2 B1679	transcription fact
29	136.5	5.8	473	2 A56175	vascular endothelial
					adhesive plaque pr

#### ALIGNMENTS

RESULT 1  
S69207  
vascular endothelial growth factor C precursor - human  
N-Alternate names: FLT4 ligand DMM  
C-Species: Homo sapiens (man)  
C-Dated: 27-Apr-1996 \*SequenceRevision: 31 Nov 1996, \*text\_change: 08-04-1996  
C-Accession: S69207, S61795, S71443, S69208, S62659  
E-Joukov, V.; Pajusola, K.; Kaipainen, A.; Chliov, D.; Laitinen, L.; Kukk, E.; Sakse  
EMBO J. 15, 1751, 1996  
A-Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand  
A-Reference number: S61795; MIMD:96203094  
A-Accession: S69207  
A-Status: nucleic acid sequence not shown  
A-Molecule type: mRNA  
A-Residues: 1-419 <300>  
A-Cross-references: EMBL:X94216, RIB:01177488, PDB:CAA3907.1, PDB:0221096, PIR:0118  
A-Note: The nucleotide sequence was submitted to the EMBL Data Library, December 1995  
A-Note: only a part of the translation is shown  
A-Note: This is a revision to the sequence from reference S61795  
E-Joukov, V.; Pajusola, K.; Kaipainen, A.; Chliov, D.; Laitinen, L.; Kukk, E.; Sakse  
EMBO J. 15, 290-298, 1996  
A-Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the FLT4  
A-Reference number: S61795; MIMD:96178224  
A-Accession: S61795  
A-Status: nucleic acid sequence not shown, not compared with conceptual translation  
A-Molecule type: mRNA  
A-Residues: 70-419 <300>  
A-Note: This sequence has been revised in reference S69207  
A-Accession: S71443  
A-Molecule type: protein  
A-Residues: 18, 104-120 <300>  
R-ecy, J.; Gray, A.; Yanc, O.; Jacob, S.M.; Aravam, H.; Wood, W.L.  
submitted to the EMBL Data Library, December 1995  
A-Description: Vascular endothelial growth factor related protein (VRP): A ligand and  
A-Reference number: S69208  
A-Accession: S69208  
A-Molecule type: mRNA  
A-Residues: 1-419 <300>  
R-Morris, J.C.  
submitted to the EMBL Data Library, May 1996  
A-Reference number: H01557  
A-Accession: G92659  
A-Status: preliminary; translated from CH/EMBL/DDB3  
A-Molecule type: mRNA  
A-Residues: 1-419 <300>  
A-Cross-references: EMBL:059111, NID:0173426, FIRM:AA09390.1, PIR:0173427  
C-Genetics:  
A-Genes: GDB:VEGFC; VRP  
A-Cross-references: GDB:3890883; OMIM:601528  
F113/Domain: signal sequence \*status predicted \*SIG>  
F113-102/Domain: propeptide \*status predicted \*PRO>







Query Match 7.44: Score 174; DB 2; Length 160;  
 Best Local Similarity 27.58; Pred. No. 6; 86-06;  
 Matches 50; Conservative 17; Mismatches 67; Indels 48; Gaps 11;

176 SNTSTSTFTFTVLSPTPTVTVSEFANLSSTNKLTVKLVNHSILP-----225  
 177 SSSNITMIMIKR---PHQSHIDHMSPLGHSWCFERKRIPIREKSNVQKQKQKPK 183  
 226 ---RSIPATVGTGVANVTTPPKNIVNNGTPTALHPPSSSLNSTSPCHTGTN 232  
 184 PRSPKRSWVHCPSPPSPKPIPVLDPTKRSK-----NTDSK-----CKAR 198  
 284 KFLPETGCG 292  
 199 QLEINERTCG 209

RESULT 9  
 J06542  
 185K secretory protein, midge (Chironomus tentans) (fragment)  
 N/AI/Genbank names: baldiant ring 3 protein  
 C/Species: Chironomus tentans  
 C/Date: 01-Dec-1991 #sequence\_revision 01-Dec-1991 #text\_change 17-Mar-2000  
 C/Accession: J06542  
 RefIDnum: S.S.; Casoy, S.T.  
 Gene 98; 133-140; 1999  
 A/Title: Baldiant ring 3 in Chironomus tentans encodes a 185 kDa secretory protein which  
 A/Reference number: J06542; M01D:90269600  
 A/Accession: J06542  
 A/Molecule type: mRNA  
 A/Residues: 1-160 112  
 A/Cross-references: GH:M24160  
 A/Experimental source: salivary gland  
 C/Superfamily: unassigned baldiant ring proteins

Query Match 7.44: Score 174; DB 2; Length 160;  
 Best Local Similarity 27.58; Pred. No. 6; 86-06;  
 Matches 50; Conservative 17; Mismatches 67; Indels 48; Gaps 11;

242 GFNVNWNQVCFELAGTEPSSHTDSSTSEFHI--CPNKEKPEPTQGVKGVK 300  
 3 CSPPQWILSKTIVCS-----IIVATCKQIWTG-----FAGCTIPQSK- 45  
 301 ISGPHKEIIVASVQVCKNKLPSSSQPKPEDEKQVCKK-----CPKHPLN 353  
 46 -MGKKKFEKPEKPKKNN--PSI--SPGVWADPEKPKPKKPKPKQDTQGGKNN 100  
 354 VAKTTPPTSPNKHGKSTSHGDS-----TPTPTVA-----NGLAGELLALV 165  
 101 DPVSPPTVPVPPPT--TNGIVNTVNTVNGVQIKPKSPVQGVYNNKRTD-----Q 150  
 406 RC 407  
 151 RC 152

RESULT 10  
 T18355  
 hypothetical protein p4 - Mycoplasma hyorhinis  
 C/Species: Mycoplasma hyorhinis  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 07-Nov-1999  
 C/Accession: T18355  
 RefIDnum: G.; McIntosh, M.A.  
 J. Infectiol. 176; 5929-5947; 1994  
 A/Title: An amplifiable DNA region from the Mycoplasma hyorhinis genome.  
 A/Reference number: Z18888; M01D:9501025  
 A/Accession: T18355  
 A/Status: preliminary; contig from DE/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-1187 <DEN>  
 A/Cross-references: EMBL:U11447; NIDB:J50156; PIR:G66056; PIR:AA62228; 1  
 C/notes:  
 A/nucleic code: SGC

Query Match 7.28: Score 170.5; DB 2; Length 1187;  
 Best Local Similarity 24.19; Pred. No. 9; 96-09;  
 Matches 69; Conservative 24; Mismatches 92; Indels 99; Gaps 17;

161 GGGGNSNEL-----GMINSTNY-----SKLLEIVLHSHQKIVISFANHS 207  
 218 GGGVANSVNCVLCESNAG--NPGQVKEVKEVKEVKEVKEVKEVKEVKEV 271  
 208 GCGSKLIVPVVSHIIRSLPATQV---HWANKTCRN-----HWNNQVCP 255  
 272 -----DHFELVH-----LHFVCLAGVHATDICKNLHSLIYKKNQVYN 316  
 256 IAGHPPTSSHGSPSPSPHITVPPNPELEDEYQGVK-----GVVNTSGPK 407  
 317 LPELELELVADSVVEGKEHVGQSKLEIHSQDPAKQCPCEKNSQSLTGG--- 373  
 308 ELHAGQGMKNKLSSNNNPEFEKNGVCKN-----GNHHLNARKTGVETS 364  
 374 -CGEATCSAQPH-----GQVEP-----SGCAPNTCACTEIR-----CTETES 412  
 365 -NGLFAGKFRHVLGSCYRPTCTVARKKDPALAEVTCV 408  
 413 -----TGGENPCRPPEACD-----SEHDECV 438

RESULT 11  
 J04680  
 vascular endothelial growth factor related factor 167 precursor - mouse  
 N/AI/Genbank names: VRF 167 protein  
 C/Species: Mus musculus (house mouse)  
 C/Date: 10-May-1996 #sequence\_revision 19 Jul 1996 #text\_change 05-Nov-1999  
 C/Accession: J04680  
 RefIDnum: S.; Iqbal et al.; J. Biol. Chem. 271; 9229-9238; 1996  
 Biochem. Biophys. Res. Commun. 229; 9229-9238; 1996  
 A/Title: Characterization of the murine VEGF related factor gene.  
 A/Reference number: J04679; M01D:96184052  
 A/Accession: J04680  
 A/Molecule type: mRNA  
 A/Residues: 1-188 <TOM>  
 A/Cross-references: GH:U43847; NID:G14335; PIR:NAC62553.1; PIR:U414346  
 C/Comment: This factor is a mitogen, that is selective for endothelial cells, and bel  
 at endothelial growth factors 167 and VEGF 186.  
 A/Genes: vrf  
 A/Map position: 19  
 A/Introns: 137/2  
 F1-21/Domain: signal sequence #status predicted -S16-  
 F1-22/Domain: vascular endothelial growth factor related factor #status predicted

Query Match 7.08: Score 164.5; DB 2; Length 188;  
 Best Local Similarity 26.08; Pred. No. 4; 0-05;  
 Matches 50; Conservative 25; Mismatches 78; Indels 39; Gaps 7;

107 KFAAHYNAELIKSLTEFWKIQMPREVVYDKEKGAIIIEFKVYVSLYKGGAN 166  
 26 GFQSGSHQKKVPMIVAPAI--QPRVYVVRISMELMGVNVKQIVSCTVWQACDGP 84  
 167 -GAGGKMSIRKIVLILIVVSGVGVVYV--ANLQVQV--NSVTVYV--VHSGT 225  
 84 DQVFRVVTGQHQVPMQIIMQVPSQAGE---MSLEHNSQCHTRPK-----KKSAVKP 145  
 226 ---RSI--FALDTGVHANKTCKPKHVVNNQJGCLAGVHPGFSHKLDSISLKGPHITG 280  
 136 DSPRILICPFCIDPRVPTPTPTCP-----CPVPR-----KPLHVGQ 171  
 281 EKKELEDTGQ 292  
 172 PGLEINERTCG 184

RESULT 12  
 S57956









Sequence version 4.5  
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0M protein - protein search, using sw model

Run on: February 20, 2002, 16:27:32 : Search time 17.06 seconds  
(without alignments)  
898 354 Million cell updates/sec

Title: US-09-534-376a-13  
Sequence: 1 MBLPMELSLQPTLAAACAVIL.....LAAEDVQVRISKRRIUM 418

Scoring table:  
BLAST/MSM6.2  
Gapop 10.0, Gapext 0.5

Searched: 100059 seqs, 46664627 residues

Total number of hits satisfying chosen parameters: 100059

Minimum hit seq length: 0  
Maximum hit seq length: 20000000

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_39.\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length (R)	ID	Description
1	1804.5	76.7	419	VEGF_HUMAN
2	1747.5	74.2	415	VEGF_MOUSE
3	241	10.2	1700	HARL_CHITE
4	199	8.5	215	VEGF_HUMAN
5	191.5	8.1	190	VEGF_PIG
6	188.5	8.0	190	VEGF_RAT
7	179.5	7.6	164	VEGF_CAVPO
8	174.5	7.4	190	VEGF_BOVIN
9	174.5	7.4	214	VEGF_MOUSE
10	169	7.2	214	VEGF_CHICK
11	164.5	7.0	188	VEGF_MOUSE
12	162.5	6.9	188	VEGF_HUMAN
13	158.5	6.7	146	VEGF_SHEEP
14	152	6.5	2871	VEGF_MOUSE
15	150	6.4	148	VEGF_GREN7
16	147.5	6.3	170	VEGF_HUMAN
17	147	6.2	2871	VEGF_PIG
18	146.5	6.2	134	VEGF_CHICK
19	144	6.1	2871	VEGF_HUMAN
20	141.5	6.0	4712	LMA_DRUM
21	141	6.0	380	SEH_MOUSE
22	140	5.9	2871	VEGF_BOVIN
23	138	5.9	812	VEGF_RAT
24	137.5	5.8	1104	VEGF_HUMAN
25	137.5	5.8	1964	VEGF_MOUSE
26	136.5	5.8	473	VEGF_MYICA
27	136.5	5.8	1808	VEGF_CHICK
28	135	5.7	2318	VEGF_MOUSE
29	134.5	5.7	2201	VEGF_HUMAN
30	134	5.7	2704	VEGF_MOUSE
31	134.5	5.7	810	VEGF_RAT
32	132.5	5.6	810	VEGF_HUMAN
33	132	5.6	919	VEGF_HUMAN

34	132	5.6	2813	VEF_CANPA	Q28295 canis fami
35	131.5	5.6	2531	VEGF_MOUSE	Q01705 mus musculi
36	131	5.6	158	VEGF_MOUSE	P49764 mus musculi
37	129.5	5.5	1106	VEGF_MOUSE	P40798 drosophila
38	129.5	5.5	1408	VEGF_MOUSE	P18168 drosophila
39	128	5.4	2813	VEF_HUMAN	P04275 homo sapien
40	128	5.4	3051	VEGF_CAEEL	P44576 caenorhabdi
41	128	5.4	5376	VEGF_MOUSE	Q88759 mus musculi
42	127	5.4	1429	VEGF_CAEEL	P14585 caenorhabdi
43	126.5	5.4	241	VEGF_SHEEP	Q67226 ovies aries
44	126.5	5.4	1877	VEGF_MOUSE	Q04592 mus musculi
45	126	5.4	575	VEGF_HUMAN	P07204 homo sapien

## ALIGNMENTS

RESULT: 1  
VEGF\_HUMAN  
ID VEGF\_HUMAN STANDARD PRI: 419 AA.  
AC P49767:  
DT 01-OCT-1996 (Ref. 34, created)  
DT 01-OCT-1996 (Ref. 34, last sequence update)  
IT 20-AUG-2001 (Ref. 40, last annotation update)  
DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (VEGF-C) (VASCULAR  
DE ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRF) (F114 LIGAND) (F114-  
DE L).  
GN VEGFC.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A. AND SEQUENCE OF 103-120.  
RX MEDLINE:96178224; PubMed:8617204;  
RA Joukov V., Pajusola K., Kalkkinen A., Chillov D., Laitinen I., Kerk E.,  
RA Saksela O., Kalkkinen N., Allitalo K.;  
RT "A novel vascular endothelial growth factor, VEGF-C, is a ligand for  
PT the Flt4 (VEGFR-3) and Klf2 (VEGFR-2) receptor tyrosine kinases";  
RL EMBO J. 15:290-298(1996).  
RN [2]  
RP EPRAFUM.  
RX MEDLINE:96203094; PubMed:8612600;  
RA Joukov V., Pajusola K., Kalkkinen A., Chillov D., Laitinen I., Kerk E.,  
RA Saksela O., Kalkkinen N., Allitalo K.;  
RL EMBO J. 15:1751-1751(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE:96319226; PubMed:870872;  
RA Lee J., Gray A., Yoon J., Lach S.M., Avraham H., Wood W.L.;  
RT "Vascular endothelial growth factor-related protein a ligand and  
RT specific activator of the tyrosine kinase receptor Flt4";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:1988-1992(1996).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX Fitz L., Morris J.C., Towler P.S., Long A.J., Grier R.,  
RA Burgess P., Giannelli J., Charleita A., Hennessy D., Kovacic S.,  
RA Fitzgerald M., Scallietto H., Welsh N., Neven S., Finerty H.,  
RA Zollner R., Wang J., Nickbarg E., Gassaway R., Turner K.,  
RA Wood C.R.;  
RT "Identification of (TNF- $\alpha$ ) to the EM6/Receptor/TNFR1 databases,  
CC - FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL  
CC CELL GROWTH.  
CC - SIMILARITY: HOMOLOG: DISULFIDE-LINKED.  
CC - SIMILARITY: PROBABLY PROBABLY PROCESSED IN THE C-TERMINUS.  
CC - SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL contribution -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see http://www.isb.ch/).  
CC



[illegible]

RESULT	3
ID	BARK_WHITE
NAME	PARK_WHITE
STANDARD:	PRF: 1700 AA.
ACC	603376;
D1	01-001-1994 (Ref.: 27; Created)
D2	01-001-1994 (Ref.: 27; Last sequence update)
D3	01-001-1994 (Ref.: 40; Last annotation update)
DE	BALHANT RING PROTEIN 3 PRECURSOR.
CN	BK1.
OS	Chironomus tentans (Midge).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
NC	Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
OX	Chironomidae; Chironomidae; Chironominae; Chironomus.
XX	NBI_Laxid_7154;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE: Salivary gland;
FX	MEDLINE 9817494; PubMed 1689777;
FA	Jacobsen G., Landahl U., Gall J., Ericsson O., Wrolander L.;
K1	The Balbant Ring 3 gene in chironomus tentans has a diverged
R1	repetitive structure split by many introns."?
KL	J. Mol. Biol. 211:341-344(1990);
G1	-1- FUNCTION: USED BY THE LARVAE TO CONSTRICT A SUPRAPHARYNGEAL STRUCTURE. THE LARVAL TIRE BALBANT RING PROTEIN 3 COULD PLAY A ROLE AS A TRANSPORT PROTEIN THAT BINDS TO OTHER PROTEINS INTRACELLULARLY AND IN THE GLAND LUMEN IN ORDER TO PREVENT THEM FROM FORMING WATER-INSECTICIDE FILIPS TOO EARLY
CC	-1- SUBCELLULAR LOCATION: SECRETED.
CC	-1- TISSUE SPECIFICITY: SALIVARY GLAND
CC	-1- DOMAIN: HAS 82 APPROXIMATE REPEATS OF CYS-X-CYS-X-CYS.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement ( <a href="http://www.ebi.ac.uk/stb/bioinformatics/">http://www.ebi.ac.uk/stb/bioinformatics/</a> ) or send an email to <a href="mailto:license@stb.ebi.ac.uk">license@stb.ebi.ac.uk</a> .
CC	-----
EMBL:	X52263; CAA36506.1; -;
DB	PIR: S08167; S08167.
DB	BSSP: P18055; ZMR8
DB	InterPro: IPR000853; M11ELI01_nemat.
DB	TrEMBL: P090876; MINEMADREF.
KW	Repeat; Signal.
FT	SIGNAL
ET	CHAIN 1 1700
SD	SEQUENCE 1700 AA: 166145 MW: 24202495.1160915 CPM64; BALBANT RING PROTEIN 3.

[illegible]

RESULT	4
VEGF_HUMAN	
ID	VEGF_HUMAN
STANDARDID	PRT
215 AA.	
AC	P15692;
DT	01-APR-1990 (rel. 14, Created)
DT	01-APR-1990 (rel. 14, Last sequence update)
DT	20-AUG-2001 (rel. 40, Last annotation update)
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE	PERMEABILITY FACTOR) (VPEF).
GN	VEGF OR VEGFA.
OS	Homo sapiens (human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OC	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=90069408; PubMed=2479987;
RA	Leung D.W., Cachianes G., Kiang J.-J., Goeddel D.V., Ferrara N.;
RT	"Vascular endothelial growth factor is a secreted angiogenic
PL	mitogen.";
PL	Science 246:1496-1499(1989).
[2]	
RP	SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX	MEDLINE=90069609; PubMed=2479987;
RA	Key J. P., Hsu S. D., Rivli S., Sasse K., Warren T., Fodor J.,
RT	Connolly D.T.;
PL	"Vascular permeability factor, an endothelial cell mitogen related to
PL	PDGF.";
PL	Science 246:1309-1312(1989).
[3]	
RP	SEQUENCE FROM N.A.
RX	MEDLINE=9126072; PubMed=1711045;
RA	Tischer E., Mitchell R., Hartman T., Silva M., Gospodarowicz D.,
RA	Fidles J.C., Abraham J.A.;
RT	"The human gene for vascular endothelial growth factor, VEGF,
RT	protein forms are encoded through alternative exon splicing.";
RL	J. Biol. Chem. 266:11947-11954(1991).
[4]	
RP	SEQUENCE FROM N.A.
RX	MEDLINE=92231879; PubMed=1567395;
RA	Weinreb K., Marne D., Weich H.A.;
RT	"Anti-associated Kaposi's sarcoma cells in culture express vascular
RT	endothelial growth factor.";
PL	Biochem. Biophys. Res. Commun. 184:1167-1174(1992).
[5]	
RP	PELLINIMARY SEQUENCE OF 27-46; 44-50 AND 59-81.
RX	MEDLINE=90062112; PubMed=2584205;
RA	Connolly D.T., Olander J.V., Neveuiman D., Nelson K., Mossell K.,

KA Sheel N., Hazmore B.L., Lemminger R., Feder J.:  
 KA human vascular permeability factor. Isolation from 0937 cells. \*  
 KA J. Biol. Chem. 264:28017-28024(1989).  
 KA [6]  
 KA SEQUENCE of 27 41.  
 KA MEDLINE 9434546; PubMed 7678805;  
 KA Kuech H.L., Jaeger R., Schoelmann C., Weindel K., Willing J.,  
 KA Koch G., Marne D., Hug B., Welch H.A.:  
 KA "Synthesis and assembly of functionally active human vascular  
 KA endothelial growth factor homologs in insect cells. \*"  
 KA Proc. Natl. Acad. Sci. U.S.A. 94:7192-7197(1997).  
 KA [7]  
 KA X RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 34-135.  
 KA MEDLINE 97552774; PubMed 9207967;  
 KA Muller Y.A., Li B., Christinger H.W., Wells J.A., Cunningham B.C.:  
 KA "de Vos A.M.:  
 KA "Vascular endothelial growth factor: crystal structure and functional  
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 DR EMBL: M64322; AAA56804.1; JOINED.  
 DR EMBL: M64323; AAA56804.1; JOINED.  
 DR EMBL: M64324; AAA56804.1; JOINED.  
 DR EMBL: M64325; AAA56804.1; JOINED.  
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 DR EMBL: M64329; AAA56804.1; JOINED.  
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 DR EMBL: M64336; AAA56804.1; JOINED.  
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 DR EMBL: M64345; AAA56804.1; JOINED.  
 DR EMBL: M64346; AAA56804.1;

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VEGF_P1:
10 VEGF_P1G STANDARD: PRT: 190 AA.
11 VEGF_P1G
12 49151)
13 01-FEB-1996 (rel. 43, created)
14 01-FEB-1996 (rel. 43, last sequence update)
15 20-APR-2001 (rel. 40, last annotation update)
16 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
17 PERMEABILITY FACTOR) (VPF).
18 VEGF.
19 Sus scrofa (Pig).
20 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
21 Mammalia; Eumetazoa; Cetartiodactyla; Suidae; Sus.
22 HBB_L1441D.9823).
23 111
24 SEQUENCE FROM N.A.
25 1150NF=Heart;
26 MEDLINE:95143284; PubMed 7841203;
27 Sharma H.S., Tani Z.H., Ghe R.C.H., Verdoux P.D.:
28 "Nucleotide sequence and expression of the porcine vascular
29 endothelial growth factor".
30 Biochim. Biophys. Acta 1268:215-238(1995)
31 -1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
32 CELL GROWTH INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
33 PERMEABILITY (BY SIMILARITY).
34 -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY)
35 -1- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO PTGS OR
36 IS THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
37 SIMILARITY).
38 -1- SIMILARITY: BELONGS TO THE VEGF/VPF FAMILY OF GROWTH FACTORS.
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	RESULT	6			
AC	VEGF_RAT		STANDARD:	PRT:	190 AA.
AC	P16612;				
DT	01-AUG-1990	(rel. 15, created)			
DT	01-AUG-1990	(rel. 15, last sequence update)			
DT	20-AUG-2001	(rel. 40, last annotation update)			
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF).				
GN	VEGF.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Genitalia; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	Nebi_Taxid=101157;				
RN	[1]				
FX	SEQUENCE FROM R.A., AND SEQUENCE OF 27-190.				
PE	MEDLINE=90207219; PUBMED 220579;				
FA	Corn G., Bayne M.L., Soderman D.D., Kwok P.W., Sullivan K.A.,				
FA	Faircliff L.M., Bivins A., Thomas K.A.;				
PT	Amino acid and cDNA sequences of a vascular endothelial cell mitogen				
RL	that is homologous to platelet-derived growth factor. <sup>2</sup>				
CC	Proc. Natl. Acad. Sci. U.S.A. 87:2628-2633(1990).				
CC	- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR PERMEABILITY.				
CC	- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.				
CC	- SUPERCELLULAR LOCATION: SECRETED; NOT REMAINS ASSOCIATED TO CELLS OR TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY SIMILARITY).				
CC	- TISSUE SPECIFICITY: EXPRESSED IN THE PITUITARY, IN BRAIN, IN PARTICULARLY IN SUPRAOPTIC AND PARAVENTRICULAR NUCLEI AND THE CHORDOID PLEXUS. ALSO FOUND ABUNDANTLY IN THE CORPUS LUTEUM OF THE OVARY AND IN KIDNEY GLOMERULI.				
CC	- SIMILARITY: BELONGS TO THE FIVE-VEGF FAMILY OF GROWTH FACTORS.				
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - between the European Bioinformatics Institute. There are no restrictions on its CC use by non profit institutions as long as its content is in no way modified and this statement is not removed, usage by and for commercial entities requires a license agreement (See http://www.ebi.ac.uk/about/every or send an email to license@sb-sib.ch).				
CC	EMBL: M32167, AAAA1211.1, ..				
DR	PIR: A35987; A35987.				
DR	HSSP: P15692; ZVGH.				
DR	InterPro: IPR00072; PDGF.				
DR	Plam: PF00441; PDGF; 1.				
DR	ProDom: PD001629; PDGF; 1.				
DR	SMART: SM00141; PDGF; 1.				
DR	PROSITE: PS00249; PDGF_1; 1.				
DR	PROSITE: PS00278; PDGF_2; 1.				
KW	Mitogen; Growth factor; Glycoprotein; Signal.				
FT	ETCAT	1	26		
FT	CHAIN	27	190		VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT	DISULFID	51	93		BY SIMILARITY.
FT	DISULFID	82	127		BY SIMILARITY.
FT	DISULFID	86	129		BY SIMILARITY.
FT	DISULFID	76	76		INTERCHAIN (BY SIMILARITY).
FT	DISULFID	85	85		INTRACHAIN (BY SIMILARITY).
FT	CAMP-HIS	109	109		N-TERMINAL (CONNA...)
SQ	SEQUENCE	190 AA;	22396 MW;	58947401041F+77 CR+64;	
Query Match	8.0%	Score 188.5;	DB 1;	Length 190;	
Best Local Similarity	22.1%;	Prod. No. 4.5e-08;			
Matches	57;	Conservative	54;	Mismatches	66;
				Indels	99;
				Gaps	10;

[illegible]

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01 Modifies 47: Conservative 32: Mismatches 68: Indels 81: Gaps
02
03 116 ELLASLHIDBRKTCGMBREYVLAKEEKGATINIPFAIVSYIYQVGGNSNIGWMMI 175
04      | : : : : : | : : : : : | : : : : : | : : : : :
05 12 EEKFMFVV YRKSVCPTLEMLVDIEVEYEFYFKSVTPMRRGVGNDSPELV 68
06
07 176 STNYSTSLPELPVPSIRCKPVTSEFNHSICRWMSKIIVYQVSH1IKRSIALQIQ 245
08      | : : : : : | : : : : : | : : : : : | : : : : :
09 69 PTEFFNTLMQIMAKRHQDGHGMSNPGRSKCGCRKKKKARQ-----ENR 116
10
11 246 EVANKPFRNNHNDLCPETAGHGFSSHGGSISPSHHOQINK ELDEFTVQ 292
12      | : : : : : | : : : : : | : : : : : | : : : : :
13 117 GRGSEFEKHIFVADPCTKSPTR-----NTISSP-----KRAQLDELNRGQ 159
14
15 RESULT #
16 VEGF_BovVIN STANDARD: PKT 140 AA.
17 ID_VEGF_BovVIN STANDARD: PKT 140 AA.
18 p15691;
19 DT 01-APR-1990 (Ref.: 14, "Created")
20 DT 01-APR-1990 (Ref.: 14, Last sequence update)
21 DT 20 AUG-2001 (Ref.: 40, Last annotation update)
22 DE VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
23 PERMEABILITY FACTOR) (VPF).
24 GN Bos taurus (bovine).
25 OS Embryonal; Metazoan; Chordata; Vertebrata; Euteleostomi;
26 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
27 Bovinae; Bovineae; Bos.
28 GC NP_01_LAIKD-9914;
29 LN [1]
30 PP SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.
31 RX MEDLINE 90069608; PubMed 2479986;
32 RA Young D.W., Cechinians G., Kuang W.-J., Goodell B.V., Fortina N.;
33 RT "Vascular endothelial growth factor is a secreted angiogenic
34 mitogen.";
35 PI Science 246:1306-1309(1989).
36 LN [2]
37 RP SEQUENCE OF 27-190 FROM N.A.
38 RX MEDLINE 9612125; PubMed 2610687;
39 RA Tischer E., Gospodarowicz D., Mitchell R., Silva M., Schilling J.,
40 Lau K., Crisp T., Fiddes J.C., Abraham J.A.;
41 RT "Vascular endothelial growth factor: a new member of the platelet-
42 derived growth factor gene family.";
43 PI Biochem. Biophys. Res. Commun. 165:1198-1206(1989).
44 LN [3]
45 RN SEQUENCE OF 27-81.
46 RX MEDLINE 89286596; PubMed 2735925;
47 RA Fortina N., Benzol W.J.;
48 RT "Primary follicular cells secrete a novel heparin binding growth
49 factor specific for vascular endothelial cells.";
50 PI Biochem. Biophys. Res. Commun. 161:851-856(1989).
51 LN [4]
52 RL FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND VASCULAR
53 CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
54 PERMEABILITY.
55 LN [5]
56 CC SUBUNIT: MONOMERIC; DISULFIDE LINKED.
57 CC -1: SUBJECT HAS LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
58 CC TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
59 CC SIMILARITY).
60 CC -1: SIMILARITY: BELONGS TO THE PDGF/VBGF FAMILY OF GROWTH FACTORS.
61 CC
62 THIS SWISS-PROT entry is copyright . It is produced through a collaboration
63 between the Swiss Institute of Bioinformatics and the EMBL institution. Its
64 use by non-profit institutions as long as its content is in no way
65 modified and this statement is not removed, disseminated for commercial
66 purposes requires a license agreement (http://www.isdb.ch/licenses/)
67 or send an email to license@isdb.ch.
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69 EMDL: M42976; AAA40502.1;
70 EMDL: M41846; AAA30804.1;
71 EMDL: M43750; AAA30805.1;
72
73 PIR: A4255; A43255.

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ET	D MAIN	449	489	EGE-LIKE 6, NON-CALCIUM BINDING
ET	D MAIN	490	529	EGE-LIKE 7, CALCIUM BINDING
ET	D MAIN	530	571	EGE-LIKE 8, CALCIUM-BINDING
ET	D MAIN	572	612	EGE-LIKE 9, CALCIUM-BINDING
ET	D MAIN	613	653	EGE-LIKE 10, CALCIUM-BINDING
ET	D MAIN	656	721	TOTBP 2,
ET	D MAIN	723	764	EGE-LIKE 11, CALCIUM-BINDING
ET	D MAIN	765	806	EGE-LIKE 12, CALCIUM-BINDING
ET	D MAIN	807	846	EGE-LIKE 13, CALCIUM-BINDING
ET	D MAIN	910	951	EGE-LIKE 14, CALCIUM-BINDING
ET	D MAIN	952	1018	TOTBP 3,
ET	D MAIN	1028	1066	EGE-LIKE 15, CALCIUM-BINDING
ET	D MAIN	1070	1112	EGE-LIKE 16, CALCIUM-BINDING
ET	D MAIN	1113	1154	EGE-LIKE 17, CALCIUM-BINDING
ET	D MAIN	1155	1196	EGE-LIKE 18, CALCIUM-BINDING
ET	D MAIN	1197	1237	EGE-LIKE 19, CALCIUM-BINDING
ET	D MAIN	1238	1279	EGE-LIKE 20, CALCIUM-BINDING
ET	D MAIN	1280	1321	EGE-LIKE 21, CALCIUM-BINDING
ET	D MAIN	1322	1362	EGE-LIKE 22, CALCIUM-BINDING
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ET	D MAIN	1487	1527	EGE-LIKE 26, CALCIUM-BINDING
ET	D MAIN	1528	1599	TOTBP 4,
ET	D MAIN	1606	1647	EGE-LIKE 27, CALCIUM-BINDING
ET	D MAIN	1648	1688	EGE-LIKE 28, CALCIUM-BINDING
ET	D MAIN	1689	1758	TOTBP 5,
ET	D MAIN	1766	1807	EGE-LIKE 29, CALCIUM-BINDING
ET	D MAIN	1808	1848	EGE-LIKE 30, CALCIUM-BINDING
ET	D MAIN	1849	1890	EGE-LIKE 31, CALCIUM-BINDING
ET	D MAIN	1891	1929	EGE-LIKE 32, CALCIUM-BINDING
ET	D MAIN	1930	1972	EGE-LIKE 33, CALCIUM-BINDING
ET	D MAIN	1973	2012	EGE-LIKE 34, CALCIUM-BINDING
ET	D MAIN	2013	2054	EGE-LIKE 35, CALCIUM-BINDING
ET	D MAIN	2055	2121	TOTBP 6,
ET	D MAIN	2127	2165	EGE-LIKE 36, CALCIUM-BINDING
ET	D MAIN	2166	2205	EGE-LIKE 37, CALCIUM-BINDING
ET	D MAIN	2206	2246	EGE-LIKE 38, CALCIUM-BINDING
ET	D MAIN	2247	2290	EGE-LIKE 39, CALCIUM-BINDING
ET	D MAIN	2291	2332	EGE-LIKE 40, CALCIUM-BINDING
ET	D MAIN	2333	2400	TOTBP 7,
ET	D MAIN	2402	2443	EGE-LIKE 41, CALCIUM BINDING
ET	D MAIN	2444	2484	EGE-LIKE 42, CALCIUM-BINDING
ET	D MAIN	2485	2523	EGE-LIKE 43, CALCIUM-BINDING
ET	D MAIN	2524	2566	EGE-LIKE 44, CALCIUM-BINDING
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ET	D MAIN	2607	2647	EGE-LIKE 46, CALCIUM-BINDING
ET	D MAIN	2648	2687	EGE-LIKE 47, CALCIUM-BINDING
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ET	D SUFF-1D	557	570	BY SIMILARITY,

DB	2343	DNRGCT
----	------	--



Thu Feb 21 09:21:40 2002

us-09-534-376a-13.rsp

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Page 13



Genforce version 4.5  
Copyright (c) 1994 - 2000 Genforce Inc.  
February 20, 2002, 15:27:08, Search time 43.31 seconds  
(without alignments)  
1411.726 Million cell updates/sec

us-09-534-376a-13

Protein: 2354

Sequence: 1 MLLLEMLSLGCTAGAGAVLL.....LLAEVGCYVTSKRPPLM 418

Scoring table:

Gapop 10.0, Gapext 0.5

Search: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPREML17:  
1: sp.archaea:  
2: sp.bacteria:  
3: sp.fungi:  
4: sp.juman:  
5: sp.invertebrate:  
6: sp.mammal:  
7: sp.abc:  
8: sp.organelle:  
9: sp.phage:  
10: sp.plant:  
11: sp.podent:  
12: sp.virus:  
13: sp.vertebrate:  
14: sp.unclassified:

Print. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2442	99.5	418	13	057352
2	1779	75.6	418	6	09X850
3	677	28.8	454	4	044915
4	566	28.3	458	11	097946
5	436.5	27.0	427	11	035251
6	556	23.6	126	11	045757
7	232	9.9	1698	5	094438
8	231	9.8	1704	5	094446
9	211.5	9.0	232	4	094129
10	211.5	9.0	254	4	014889
11	202	8.6	208	4	09X854
12	202	8.6	259	4	060720
13	198.5	8.5	214	6	09X855
14	198.5	8.4	214	6	09X853
15	196	8.3	122	6	0941X1
16	194.5	8.3	190	6	09X853
17	193.5	8.2	190	6	09X850
18	186.5	7.9	190	6	094152
19	186.5	7.9	190	11	09X839

20	184	7.8	191	4	075875
21	184	7.8	194	13	042572
22	183.5	7.8	194	4	094123
23	180.5	7.7	190	6	077643
24	175	7.4	171	4	0941W8
25	174.5	7.4	214	11	09X807
26	174	7.4	190	11	09X851
27	172	7.3	147	4	090858
28	170.5	7.2	1187	2	049549
29	170	7.2	142	11	09X856
30	169.5	7.2	188	13	074682
31	167.5	7.1	124	6	09X800
32	167.5	7.1	150	11	034881
33	165.5	7.0	314	5	0948X1
34	164.5	7.0	704	3	074567
35	163	6.9	126	6	094807
36	161.5	6.9	188	6	09X848
37	161.5	6.9	301	5	09X8P6
38	158.5	6.7	118	6	09X8H1
39	156.5	6.6	148	13	042571
40	156.5	6.6	170	11	0948X7
41	156.5	6.6	800	5	09X878
42	152.5	6.5	146	11	09X8C6
43	152.5	6.5	442	7	044247
44	151	6.4	123	6	0941S1
45	149.5	6.4	170	4	09X878

## ALIGNMENTS

RESULT	ID	1	PRELIMINARY:	197:	418 AA.
057352	057352				
AC	057352				
DT	01-JUN-1998	(TEMBREL. 06, created)			
DT	01-JUN-1998	(TEMBREL. 06, last sequence update)			
DT	01-JUN-2001	(TEMBREL. 17, last annotation update)			
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR.				
GN	VEGF-C.				
OS	Coturnix coturnix japonica (Japanese quail).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;				
OC	Coturnix				
OX	NCBI_TaxID:91934;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
FX	MEDLINE:98167900; PubMed:9435294;				
FA	Fitchman A, Cortez C, Jaitre T, Breat V, Joukov V, Kumar V,				
RA	Allato K, Le Douarin N.M.;				
RT	"Avian VEGF-C: cloning, embryonic expression pattern and stimulation				
RT	of the differentiation of VEGFR2-expressing endothelial cell				
RT	precursors."				
RL	Development 125:743-752(1998).				
FE	EMBL: Y1837; XA75799.1; -				
DE	HSSP: P15692; IVPB				
DR	InterPro: IPR02400; GP_cysknut.				
DR	InterPro: IPR00476; Glyco_hormone.				
DR	InterPro: IPR00672; PDGF.				
DR	Pfam: PF0341; PDGF_1.				
DR	PRINTS: PR00438; GPCYSKNUT.				
DR	PRODOM: P0001629; PDGF_1.				
DR	SMART: SM00067; GHA_1.				
DR	SMART: SM00141; PDGF_1.				
DR	PROSITE: PS00249; PDGF_1; 1.				
DR	PROSITE: PS00278; PDGF_2; 1.				
DR	Signal.				
KW	Signal.				
FT	CHAIN	1	31	POTENTIAL.	
FT	CHAIN	111	418	VASCULAR ENDOTHELIAL GROWTH FACTOR C.	
SO	SEQUENCE	418 AA;	40839 MW;	0948077451H2H CH764;	

Query Match

99.5% Score 2342; DB 13; Length 418;









```

SEQUENCE FROM N.A.
AC TISSUE-SALIVARY GLAND
AC Case S.T. Gray C. Holt W.C. Hoffman E.T. Martin J. Hamilton R.J.
BL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: H54641: AAA49804.1:
DR InterPro: IPR000561: EGF-like.
DR InterPro: IPR000853: Multihelium_domain.
DR PRINTS: PR00876: MTNEMAD00F.
DR PROSITE: PS00022: FGF_1: FGF_1_1:
DR PROSITE: PS01186: EGF_2: UNKNOWN_1.
DR PROSITE: PS02441: FGF_1:
SEQUENCE: 1794 AA: 185745 MW: 34526217381228 CRR611.

Query Match 9.98: Score 231; Db 5; Length 1704;
Best local similarity 19.78; Pred. No. 1.6e-13;
Matches 90; Conservative 52; Mismatches 192; Indels 122; Gaps 17;

UY EEDRAGPEPRKASHKIDFQLPSSVSDPIMTVIPPEWMEKQLPKGWMJNPHSS 98
DB 963 DEMONKSPFAWSHPTTRKAKNATATVA---EYMLNLC---KQDIAKQMTVA 1016
UY 54 ITRSDLSIKFAAHYNAFIIKSDTPWPKTQ-----MPEPVVDLQK--- 141
DB 1017 ENKREDAITSCVGRKSP--MISVLEGRKNNETGALGVANGCKAPQRMIDNICKTC 1074
UY 142 -----EKGATNTEPRKPSYK-----GGGNSHGLQGMISTN 178
DB 1075 PUVNTNPAKQTEPSETPKCTF---KIKLIDPFPSNLEKQVQDQKCKQKQIFDK 1130
UY 179 YISKTELEITVP-----LSHGRKPVTV---VSFANHSCKQMSKLDVY 217
DB 1141 NICKCKPPEKPKPCKKPKKPKKPKKPKKPKKPKKPKKPKKPKKPKKPKKPKK 1190
UY 218 KQV-----HSTRSLATLQCHVAN-----KCTKHNNVNDI 252
DB 1191 KTRPRGKNNWQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQ 1250
UY 253 GPTLAQHDPESSHIGSDTSEGHIGGPFLEDEIQVCKGVPRISGHIQKIDPA 312
DB 1251 GVVV-----PKNPKRANQ--NKKNNIKACPEPKPKPKPKPKPKPKPKPKPK 1298
UY 313 SCQKMG-KNKIPSSQPKPEFPEPKQV-VYKKT-----QPKHPI NPAKQTEPESFN 366
DB 1299 TCAECPEPKALFASQDQKSWNDQSVCKSKMPKQKQKQKQKQKQKQKQKQKQKQ 1356
UY 367 KPLKPKKPHHQTGCVPRPVTKPKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQ 408
DB 1357 QTCPAQSWISQTCQSCP-----ATKCTTAQPKWAKQKQV 1394

RESULT 9
ID U9H1W9 PRELIMINARY; PRT: 232 AA.
AC U9H1W9;
DT 01-MAR-2001 (TEMBUREL, 16, Created)
DT 01-MAR-2001 (TEMBUREL, 16, Last sequence update)
DT 01-JUN-2001 (TEMBUREL, 17, Last annotation update)
DT 01-JUN-2001 (TEMBUREL, 17, Last annotation update)
DB 0161523.6.3 (VASCULAR ENDOTHELIAL GROWTH FACTOR).
GN VEGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID:9606;
RA Mammalia;
RP SEQUENCE FROM N.A.
RA Williams S.J.
BL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL16141: CAC19612.1:
DR InterPro: IPR000072: PDEF
DR Pfam: PF00441: PDEF_1.
DR Pfam: PF001629: PDEF_1.
DR SMART: SM00441: PDEF_1.
DR PROSITE: PS00249: PDEF_1:
SEQUENCE: 254 AA: 24461 MW: 06999989724988 CRR64.

```

```

DR PROSITE: PS0278: PDEF_2: 1.
SQ SEQUENCE 232 AA: 27042 MW: 3452644464D01 CRR64.

Query Match 9.98: Score 211.5; Db 4; Length 254;
Best local similarity 24.28; Pred. No. 1.4e-12;
Matches 68; Conservative 43; Mismatches 105; Indels 75; Gaps 10;

UY 68 LMTVATLWMEKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQ 127
DB 14 LMTVATLWMEKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQ 149
UY 128 TQSMPEPVYVIGKEPATNTEPRKPSYK-----GGGNSHGLQGMISTN 187
DB 50 SYCHPPTLVHIFQVPEPTFYTEKQCVQIMVQVQVQVQVQVQVQVQVQVQVQVQVQV 109
UY 188 TVPLSHGRKPVTVIPPEWMEKQLPKGWMJNPHSS 247
DB 110 K--H--H--H--H--H--H--H--H--H--H--H--H--H--H--H--H--H--H--H 162
UY 248 WNNQI--GPTLAQHDPESSHIGSDTSEGHIGGPFLEDEIQVCKGVPRISGHIQKIDPA 299
DB 163 MSVVGARQKQIM-----PWSLPGHPCGQSEKHKHLPVQDQKQKQKQKQKQKQKQKQ 207
UY 300 PISQPKPKPDPAQCVWCKNKIPSSQPKPEFPEPKQV-VYKKT-----QPKHPI 340
DB 208 -----NTSKCKAKQI-----ELNTERQK 227

RESULT 10
ID Q16889 PRELIMINARY; PRT: 254 AA.
AC Q16889;
DT 01-NOV-1996 (TEMBUREL, 01, Created)
DT 01-NOV-1996 (TEMBUREL, 08, Last sequence update)
DT 01-JUN-2001 (TEMBUREL, 17, Last annotation update)
DB 0161523.6.3 (VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)).
GN VEGF 206.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID:9606;
RA Mammalia;
RP SEQUENCE FROM N.A.
RA MEDLINE-92168017; PubMed-1794841;
RA Houck K.A., Ferrara N., Winer J., Cachianes G., Li H., Lomax D.W.;
PT "The vascular endothelial growth factor family: Identification of a
PT fourth molecular species and characterization of alternative splicing
PT of RNA."
PL Mol. Endocrinol. 5:1806-1814(1991).
DR EMBL: S85192: AAC63102.1:
DR EMBL: S85224: AAC63101.1:
DR EMBL: S85199: AAC63101.1: JOINED.
DR EMBL: S85201: AAC63101.1: JOINED.
DR EMBL: S85219: AAC63101.1: JOINED.
DR EMBL: S85222: AAC63101.1: JOINED.
DR HSPG: P15692: VPEF.
DR InterPro: IPR000872: PDEF.
DR Pfam: PF00441: PDEF_1.
DR Pfam: PF001629: PDEF_1.
DR SMART: SM00441: PDEF_1.
DR PROSITE: PS00249: PDEF_1:
DR PROSITE: PS0278: PDEF_2: 1.
FT NON-TER
SQ SEQUENCE 254 AA: 24461 MW: 06999989724988 CRR64.

Query Match 9.98: Score 211.5; Db 4; Length 254;
Best local similarity 24.28; Pred. No. 1.6e-12;
Matches 68; Conservative 43; Mismatches 105; Indels 75; Gaps 10;

UY 68 LMTVATLWMEKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQ 127

```

DB 46 LITVILYHAKMSQAAVMAKGGGQNH -----EVKRFMV YOR 71  
 QY 128 TQGMREYVYLGKREKATNTTTPKPVSYLYGGGSEGLGCMNISTNYSKTLEF 187  
 DB 72 SYGHTITLTVOLFOYVPELEYTKRPSVPLMRGGGNGNEGLCVTERPSNTFMQIMK 131  
 QY 188 TVPLSHGKRVTVSANTSTGMSKIDVYGVHSILKRSIALVLOLVYVANNV 247  
 DB 142 KP HQYQHTGEMSTLQNNKTPKPKAVAGKRSVGR - GKQKRSKRSK 184  
 QY 248 WNNQI CTETAGHGFSSHLSHSDISSECHGCKE -----LDEETGVWKGAVR 299  
 DB 185 MSYVWZAKVLM -----FWSLGHGPHVGRSHGRHGVAGVGVKSSCK - 229  
 QY 400 PLSGHEKELKASGVGKKNKLSSGKNEDEKGV 440  
 DB 240 NUSGKKAQUL -----ELNERTGV 249

## RESULT 11

Q9XSP4

PRELIMINARY: PRT: 208 AA.

01 NOV 1999 (FEBMAY 12, created)  
 01 NOV 1999 (FEBMAY 12, last sequence update)  
 01 JUN 2001 (FEBMAY 17, last annotation update)  
 06 VASCULAR ENDOTHELIAL GROWTH FACTOR 182.

CN

VASC.

CANTIS family (loop).

CANTIS: Metazoa: Chordata: Taniata: Vertebrata: Endothelium:

Mammalia: Eutheria: Carnivora: Fissipedia: Canidae: Canis.

NCBI TaxID: 96152

SEQUENCE FROM N.A.

RC TISSUE HEART

RC Tissue HEART

RC Submitted (MAR 1999) to the EMBL/GenBank/JDBI databases.

RC EMBL: AF164249; GenBank: AF029683.1

RC HSSB: P15692; VAMP

RC InterPro: IP000072; PROTE

RC Pfam: PF00341; PROTE 1

RC ProDom: PD001629; PROTE 1

RC SMART: SM00141; PROTE 1

RC PROSITE: PS00249; PROTE 1

RC PROSITE: PS50278; PROTE 2

RC SIGNAL: 208 AA; 24409 MW; Q17AC591PSC2MBE (30764)

SQ

Query Match: H:68; Score 202.5; DB 6; Length 208

Best Local Similarity: 24.68; Pred. No. 9, 96-12

Matches: 96; Conservative: 28; Mismatches: 77; Indels: 74; Gaps: 7

QY 112 TQGMREYVYLGKREKATNTTTPKPVSYLYGGGSEGLGCMNISTNYSKTLEF 171  
 DB 112 TQGMREYVYLGKREKATNTTTPKPVSYLYGGGSEGLGCMNISTNYSKTLEF 171  
 QY 44 IKHIVVAFMV YGRSGKRETLTVOLFOYVPELEYTKRPSVPLMRGGGNGNEGLCV 92  
 DB 44 IKHIVVAFMV YGRSGKRETLTVOLFOYVPELEYTKRPSVPLMRGGGNGNEGLCV 92  
 QY 172 TVPLSHGKRVTVSANTSTGMSKIDVYGVHSILKRSIALVLOLVYVANNV 247  
 DB 172 TVPLSHGKRVTVSANTSTGMSKIDVYGVHSILKRSIALVLOLVYVANNV 247  
 QY 93 G VTEREENTMOMIKRPLGQHTGEMSTLQNNKTPKPKAVAGKRSVGR - GKQKRSKRSK 147  
 DB 93 G VTEREENTMOMIKRPLGQHTGEMSTLQNNKTPKPKAVAGKRSVGR - GKQKRSKRSK 147  
 QY 248 WNNQI CTETAGHGFSSHLSHSDISSECHGCKE -----LDEETGVWKGAVR 299  
 DB 248 WNNQI CTETAGHGFSSHLSHSDISSECHGCKE -----LDEETGVWKGAVR 299  
 QY 400 PLSGHEKELKASGVGKKNKLSSGKNEDEKGV 440  
 DB 400 PLSGHEKELKASGVGKKNKLSSGKNEDEKGV 440  
 QY 173 QHGVGKRSK -----ELNERTGV 204  
 DB 173 QHGVGKRSK -----ELNERTGV 204

## RESULT 12

Q9XSP4

PRELIMINARY: PRT: 209 AA.

01 NOV 1999 (FEBMAY 12, created)

DB 01 MAY 1998 (FEBMAY 07, created)  
 DB 01 MAY 1999 (FEBMAY 19, last sequence update)  
 DB 01 JUN 2001 (FEBMAY 17, last annotation update)  
 DB VEGF183 PROTEIN PROTECTOR (VASCULAR ENDOTHELIAL GROWTH FACTOR 183)  
 DB (D126162.6.6) (VASCULAR ENDOTHELIAL GROWTH FACTOR)  
 DB VEGF  
 DB Homo sapiens (Human)  
 DB Eukaryota: Metazoa: Chordata: Taniata: Vertebrata: Endothelium:  
 DB Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.  
 DB NCBI TaxID: 96062  
 DB 11  
 DB SEQUENCE FROM N.A.  
 DB RC TISSUE KIDNEY  
 DB MEDLINE: 9906474; PubMed 987851  
 DB Vol J., Jiana A., Pol D.,  
 DB "Identification and characterization of a new splicing variant of  
 DB vascular endothelial growth factor VEGF183,"  
 DB Biochem. Biophys. Acta, Gene Struct. Expr. 1443:400-406 (1998).  
 DB 121  
 DB SEQUENCE OF 114-209 FROM N.A.  
 DB RC TISSUE-RETINA  
 DB RC Tissue-RETINA  
 DB Submitted (MAY 1998) to the EMBL/GenBank/JDBI databases.  
 DB 131  
 DB SEQUENCE FROM N.A.  
 DB RC WILLIAMS S.  
 DB Submitted (DEC-2000) to the EMBL/GenBank/JDBI databases.  
 DB EMBL: AJ010438; GenBank: CA009179.1  
 DB EMBL: AF062645; GenBank: AF06780.1  
 DB EMBL: AL146131; GenBank: CA19514.1  
 DB HSSB: P15692; VAMP  
 DB InterPro: IP000072; PROTE  
 DB Pfam: PF00341; PROTE 1  
 DB ProDom: PD001629; PROTE 1  
 DB SMART: SM00141; PROTE 1  
 DB PROSITE: PS00249; PROTE 1  
 DB PROSITE: PS50278; PROTE 2  
 DB SIGNAL  
 DB CHAIN: 1 26 POTENTIAL  
 DB SIGNAL: 27 209 VEGF183 PROTEIN  
 DB SEQUENCE: 209 AA; 24422 MW; F01GCEAN794506CA (30764)  
 SQ

Query Match: H:68; Score 202; DB 4; Length 209  
 Best Local Similarity: 22.58; Pred. No. 1, 16-11  
 Matches: 63; Conservative: 25; Mismatches: 92; Indels: 96; Gaps: 8

QY 68 LITVILYHAKMSQAAVMAKGGGQNH -----EVKRFMV YOR 49  
 DB 68 LITVILYHAKMSQAAVMAKGGGQNH -----EVKRFMV YOR 49  
 QY 128 TQGMREYVYLGKREKATNTTTPKPVSYLYGGGSEGLGCMNISTNYSKTLEF 187  
 DB 128 TQGMREYVYLGKREKATNTTTPKPVSYLYGGGSEGLGCMNISTNYSKTLEF 187  
 DB 50 SYGHTITLTVOLFOYVPELEYTKRPSVPLMRGGGNGNEGLCVTERPSNTFMQIMK 109  
 QY 188 TVPLSHGKRVTVSANTSTGMSKIDVYGVHSILKRSIALVLOLVYVANNV 247  
 DB 188 TVPLSHGKRVTVSANTSTGMSKIDVYGVHSILKRSIALVLOLVYVANNV 247  
 DB 110 KP HQYQHTGEMSTLQNNKTPKPKAVAGKRSVGR - GKQKRSKRSK 160  
 QY 248 WNNQI CTETAGHGFSSHLSHSDISSECHGCKE -----LDEETGVWKGAVR 299  
 DB 248 WNNQI CTETAGHGFSSHLSHSDISSECHGCKE -----LDEETGVWKGAVR 299  
 DB 161 -----GKQKRSKRSK 184  
 QY 401 PLSGHEKELKASGVGKKNKLSSGKNEDEKGV 440  
 DB 401 PLSGHEKELKASGVGKKNKLSSGKNEDEKGV 440  
 DB 185 -----NUSGKKAQUL -----ELNERTGV 204



Index from 192 to 192

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuLink Ltd.

# OM protein - protein search, using SW model

Run on: February 20, 2002, 16:25:45 ; Search time 42.36 seconds

(without alignments)  
730,940 Million cell updates/sec

Title: US-09-534-376A-13

Percent score: 23.4

Sequence: 1 MHLLPMSTGGTAAACAVII

11AEPVWPVPTWPEPLMN 418

Scoring tables:

Matrix: BLOSUM62

Gap: 10.0, expect 0.5

Scored: 522463 seqs, 7467320 positions

Total number of hits satisfying chosen parameters: 522463

Minimum E8 seq length: 0

Maximum seq length: 2000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

A: Geneseq\_1101:  
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2: /SIBSR/genetata/geneseq/geneseq/AA1981.DAT\*  
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21: /SIBSR/genetata/geneseq/geneseq/AA2000.DAT\*  
22: /SIBSR/genetata/geneseq/geneseq/AA2001.DAT\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2.454	100.0	418	18	AAW00934
2	2.454	100.0	418	19	AAW57543
3	1804.5	76.7	419	18	AAW17847
4	1804.5	76.7	419	18	AAW00932
5	1804.5	76.7	419	19	AAW57540
6	1804.5	76.7	419	20	AAW66203
7	1804.5	76.7	419	21	AAW10648
8	1804.5	76.7	419	21	AAW59048
9	1804.5	76.7	419	21	AAW70749
10	1804.5	76.7	419	21	AAW70982
11	1804.5	76.7	419	22	AAW17905

12	1795.5	76.3	419	18	AAW13833	Human vascular end
13	1794.5	76.2	419	20	AAV30518	Vascular endothel
14	1794.5	76.2	419	20	AAV22320	Full length human
15	1794.5	76.2	419	21	AAV97144	Vascular endothel
16	1794.5	76.2	419	22	AAV97570	Human VEGF-C prote
17	1793.5	76.2	419	19	AAW75751	Vascular endothel
18	1791.5	76.1	419	18	AAW11478	Human vascular end
19	1759.5	74.7	399	20	AAW86237	Human VEGF-C full
20	1747.5	74.2	415	19	AAW57542	Mouse VEGF-C and
21	1742.5	74.0	415	18	AAW00934	Mouse Flt4 receptor
22	1604	68.1	350	20	AAV30519	A truncated vascular
23	1604	68.1	350	20	AAV22331	Truncated human VE
24	1604	68.1	350	21	AAV97335	Truncated vascular
25	1604	68.1	350	22	AAV97577	Human VEGF-2 prote
26	1599	67.9	350	16	AAW82486	Human VEGF-C full
27	1453	61.7	318	20	AAV08284	Human growth facto
28	1417	60.2	307	20	AAW86232	Human VEGF-C full
29	1391	59.1	302	20	AAW86233	Human VEGF-C full
30	1370	58.2	297	20	AAW86234	Human VEGF-C full
31	1343	57.1	292	20	AAW86235	Human VEGF-C full
32	677	28.8	325	19	AAW62240	Human VEGF-C full
33	677	28.8	325	22	AAV97572	Human VEGF-C full
34	677	28.8	354	19	AAW49036	Human VEGF-C full
35	677	28.8	354	19	AAW61341	Human VEGF-C full
36	677	28.8	354	19	AAW44293	Human VEGF-C full
37	677	28.8	354	21	AAW10649	Human VEGF-C full
38	677	28.8	354	21	AAW29049	Human VEGF-C full
39	677	28.8	354	21	AAV70750	Human VEGF-C full
40	677	28.8	354	21	AAV70983	Human VEGF-C full
41	677	28.8	354	22	AAV70753	Human VEGF-C full
42	677	28.8	354	22	AAW47606	Human VEGF-C full
43	677	28.8	354	22	AAW70985	Human VEGF-C full
44	667.5	28.4	337	20	AAV08286	Human growth facto
45	667.5	28.4	337	20	AAW61342	Human growth facto

## ALIGNMENTS

RESULT 1

AAW00934 standard, Protein 418 AA.

AAW00934:

10-NOV-1997 (11:57:00)

Query: Flt4 receptor tyrosine kinase ligand VEGF-C.

VEGF-C, Flt4 receptor tyrosine kinase, VEGF-C, query:

endothelial growth factor receptor-3, ligand:

endothelial growth factor-3, ligand:

endothelial growth factor-3, ligand:

endothelial growth factor-3, ligand:

endothelial growth factor-3, ligand:

endothelial growth factor-3, ligand:

endothelial growth factor-3, ligand:

endothelial growth factor-3, ligand:

endothelial growth factor-3, ligand:

endothelial growth factor-3, ligand:

endothelial growth factor-3, ligand:

endothelial growth factor-3, ligand:

PI PI4 receptor tyrosine kinase ligand and related nucleic acid - used  
PT to modulate growth of endothelial cells and for diagnosis of  
PI endothelial cell diseases

Example 20:  $\text{Feaq} = 1.26 \cdot 10^{-7}$ ;  $\text{Baq} = 1.83 \text{ ppb}$ ;  $\text{Baq} / \text{Feaq} =$

Thus, F440p101, a sequence-complexed guill VEGF-c, a novel ligand that binds specifically to the F114 receptor tyrosine kinase (VEGFR-3), stimulating phosphorylation of the receptor, and which modulates the growth of endothelial cells. The sequence was deduced from a cDNA clone (F4403.00) obtained from a guill cDNA library, and shows a high degree of homology to novel, cloned human VEGF-c (GenBank U9142) and mouse (GenBank U9143) VEGF-c. recombinant guill VEGF-c polypeptides can be produced that correspond to non-human mammalian variants of VEGF-c.

500 300 100 0

Query Match	100.0%	Score	2.554	DB	18	Length	418
Best Local Similarity	100.0%	Prod. No.	2,80-188				
Matched	418	Conserved	0	Mismatches	0	Indels	0
						Caps	0

07	1	MLLEMLLSLQVLAZAVLILLLHPOHVAALHSJHUYEEHJLALCHLKAHNSKQLEFQIR	60
10	4	mllemlslsqvlaazvllllhpo hvaaahsjhuyeeehj lalchlkahnskql e f q i r	60
07	64	SVSSVSLPRLVLYYVWMLKLVGLKSLWMLNHLHSSSLQVSLQSLKLAAYANLKLNS	120
10	64	svssvslp rlvlyywmlklv glkslwmln hlhs slsqvslqslk laayanklns	120
07	124	HTFHWKLGZMRVWVGLKLFKLVGLNLPLKLVSLYTRGLGCTNSRLQVNNLSINY	180
10	124	htfhwk lgzmrvwv glklfk lvgl nlp lk lvsl ytr gl gctn srlq vnnlsiny	180
07	184	SKMLRLFLYVSLHGVYVSLVANSLSLQSLKSLVLYPVCHLSLPSLQALDGLGVANK	240
10	184	skmlrl fl ysl hgv ysl v an sl slqsl ksl v ly p ch lsl p sl q al d gl gv ank	240
07	244	TPKRNWVWNNQVGLQVLAQHPVSSSLHSLQSLSTSHPLHLCQPKNELDEETQVCKGVNP	300
10	244	tpk r n w v w n n q v g l q v l a q h p v s s l h s l q s l s t s h p l h l c q p k n e l d e e t q v c k g v n p	300
07	304	LSVGLRRLKRLKASQVWVKNKLHSSQVSKLPLPLKLVGLVKNVTKRHHPLNIAKSLTCE	360
10	304	lsvglrrl krlkasqvwv knklhssq vsklpl pl kl lvgl vknv tk r h h pl n i a k s l t c e	360
07	364	CTSSNKGCEKCKKQHHQVSLYRPLVTVPKRGLVAGLGLAEVCEVETSCKRPLNM	418
10	364	ctssnkgce kckkqh hqv sl y r pl v t v p k r gl v a g l g l a e v c e v e t s c k r p l n m	418

1000


NEW/old standard;  $\text{Protein} \times \text{AA}$

ANAL. Calcd for  $C_{10}H_{10}O$ : C, 88.10%; H, 7.39%. Found: C, 88.1%; H, 7.4%.

**THE UNIVERSITY OF CHICAGO**

COULD "CONSTITUTIONAL" GROWTH BE PROTECTED?

[illegible][illegible]

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1979, 1988, 1998.

[illegible]

XX  
PR 05-FPH-1997-9705-0795430

PA (UOW) - LUMINOUS CENTER RES.  
PA (UOHH) - UNIV HELSINKI LICENSING LTD

PI Alitalo K, Joukov V;  
XX

WPI; 1998-437470/37.

XX  
XX  
New York and London: Routledge, 1991.

used to develop procedures for analyzing

PT Transplantation  
XX

Example 20; Page 121-123; 17/pp; Eqn 15h

00 The vascular endothelial growth factor (VEGF) polypeptides have  
01 activities affect growth and migration of vascular endothelial cells,  
02 promoting growth of lymphatic endothelial cells and lymphatic vessels,  
03 increasing vascular permeability, and affecting myelopoiesis. The  
04 products can be used for stimulating and/or enhancing, for inhibiting  
05 and/or decreasing, for stimulating lymphangiogenesis, treatment or prevention  
06 of inflammation, edema, elephantiasis, or Milroy's disease. They can  
07 also be used to modulate myelopoiesis, e.g., treating granulocytopenia.  
08 They can also be used for modulating the growth of endothelial cells.  
09 They can also be used to stimulate lymphocyte production and maturation,  
10 and to promote or inhibit trafficking of leukocytes between tissues and  
11 lymphatic vessels or to affect migration in and out of the thymus.

Sequencia 418 AA

Query Match	100.0%	Score 2354	146 19	Length 418
Best Local Similarity	100.0%	Prod. No. 2,80-188		
Matches 418	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	1	MIEMSLACCTCAANAVILCEHOPVAAAYESJHYYEEENZACREKAMASKQLEELR	60
Db	1	mbhlemslacclaaavvltrpppdaayesdhnyeeepaaqepkshskileeqtr	60
QY	61	SVSSVDELMEVLYPYWYMWKCYVLRKQWQJHKEHSSDSIKSDISAKAAAYANEIKRS	120
Db	61	svssvdelmvlvpywkmkcyqlrkqwjhkehssdsiksdiskaaayaneikrs	120
QY	121	LITHEKKTQGMREVVVLAKREKANTIRTEPKYVNSTWCGVCSNSELGQMNISTNYI	180
Db	121	lithekkrtqgmrvvvlakrekantirtepkvynstwcgvcsnselegqmnsitny	180
QY	181	SKTLEFETVHLNIGKRPVYSANHNSIRKMSKIDVYKOVHSIKRSIDALVIGVIVANK	240
Db	181	sktlefetvhlngkrpvyvanhnsirkmskidvykovhsikrsidalvlgvivank	240
QY	241	YCTPETHVWNNQYVTKTAAQWDETSNQLDSTNSGQHPVYGNRELEDEETGQWQVWYKVP	300
Db	241	ycpethvwnnyvtrkaqdetsnqldstnsgqhpvygnreledeetgqvwykvrp	300
QY	301	TSQVTEHRELEKANSQYMTRELLDSTNSGQHPVYGNRELEDEETGQWQVWYKVP	360
Db	301	tsqvtehrelasqymtrlldstnsgqhpvygnreledeetgqvwykvrp	360
QY	361	GTSSPPKQELKQKREHNGVCSNYKRPVYVKRQVATVLLAEVWCVYSKRIKQIM	420
Db	361	gtssppkqelkkrrehngvcsnykrpvvykrqvattvllaevwcvyskrikim	420

天竺山

11) AAW17837 standard; Protein: 41% AA

A17 22W178472











KW Human receptor tyrosine kinase; RTK; F114; fms-like tyrosine kinase 4;  
 KW VEGFR-4; vascular endothelial growth factor receptor-4; chromosome 9q35;  
 KW cytosolic tyrosine phosphorylating enzyme; tyrosine kinase; diacylglycerol  
 KW neoplastic disease; lymphoma; carcinoma; breast; squamous cell; melanoma;  
 KW sarcoma; malignancy; VEGF-C; vascular endothelial growth factor C;  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..31  
 FT /Label= Signal peptide  
 FT 32..103  
 FT /Label= N-terminal peptide  
 FT /note= "Cleavage of this peptide from partially processed  
 VEGF-C produces a fully processed mature form of VEGF-C  
 of 21-23 kD which has high affinity to VEGFR-2"  
 FT 104..227  
 FT /Label= Mature\_VEGF-C  
 FT 228..419  
 FT /Label= C-terminal peptide  
 FT /note= "Has a pattern of spaced cysteine positions  
 reminiscent of a baiting ring 4 protein (BRP) sequence;  
 cleavage of signal peptide and the C-terminal  
 peptide produces a partially processed form of VEGF-C of  
 about 29 kD which has high affinity to F114 (VEGF-3)"  
 FT 114..213  
 FT Binding-site /note= "114-213 and signal seq. VEGF-C motif 114-213  
 at position 196 is essential for VEGFR-2 binding and at  
 195 is essential for VEGFR-2 and VEGFR-3 binding"  
 FT 131..211  
 FT /note= "Important for VEGF-C activity"  
 XX  
 XX W6200021540-A1  
 XX  
 PD 20-APR-2000.  
 XX  
 PF 08-OCT-1999; 99WO-US24525.  
 XX  
 PR 09-OCT-1998; 98US-0169079.  
 XX  
 PA (LUDWIG) Ludwig INST CANCER RES.  
 PA (OYHE-) ONYV HELSINKI LICENSING LTD OY.  
 XX  
 PI Alltalo K, Kaipainen A, Valtola K, Jussila L;  
 WP1: 2000-07450/27.  
 XX  
 LX  
 PT Treating neoplastic diseases such as lymphoma, carcinoma, melanoma  
 PT and sarcoma; involves administering a compound capable of inhibiting  
 PT binding of ligand proteins to fms-like tyrosine kinase-4 receptor -  
 XX  
 XX Example 15-17; page 140-142; 14pp; English.  
 XX  
 OS The patent discloses a method to treat neoplastic disease characterised  
 OS by expression of fms-like tyrosine kinase-4 (F114) receptor (also  
 OS referred as vascular endothelial growth factor receptor-4, VEGFR-4) in  
 OS endothelial cells of blood vessels adjacent to malignant neoplasm. The  
 OS method involves administering a compound that inhibits binding of a  
 OS ligand to F114 thereby inhibiting F114 mediated proliferation of vascular  
 OS endothelial cells. The compound is useful for treating neoplastic disease  
 OS such as breast carcinoma, squamous cell carcinoma, lymphoma, melanoma  
 OS and sarcoma. F114 receptor tyrosine kinase binding compounds can be used  
 OS for manufacturing medicament useful for diagnostic screening, imaging and  
 OS treatment of malignancies characterised by F114-expressing blood cells.  
 OS The F114 gene maps to chromosome region 9q35 and is expressed as 5.8 kb  
 OS and 4.5 kb mRNAs which differ in their 3' sequences and are  
 OS differentially expressed in HEK and DAMI cell lines. F114  
 OS belongs to a subfamily of class III receptor tyrosine kinases (RTKs).  
 OS It is used as a target for tumor imaging and anti-tumor therapy.  
 OS The present sequence is a human prepro vascular endothelial growth  
 OS factor C (VEGF-C), a specific example of F114 binding compound.  
 XX  
 XX Sequence 419 AA:

Query Match 76.7% Score 1804.5; ID 21; Length 419;  
 Best Local Similarity 75.7%; Pred. No. 196-142;  
 Matches 318; Conservative 0%; Mismatches 60; Indels 5; Gaps 4;  
 QY 1 MALLKMLSLVETVLAAGAVITGPGVPPVAAAPSPSGHYVPPPPAPKAPKAKSKHLEPOL 59  
 DB 1  
 QY 60 PPSVSVDEIMTVLYPEYWKMKKQVFKKAWHNPSSSTPSPDSKFAAAHYNAATIK 119  
 DB 1  
 QY 61 PPSVSVDEIMTVLYPEYWKMKKQVFKKAWHNPSSSTPSPDSKFAAAHYNAATIK 120  
 DB 1  
 QY 126 STTEPKRPGMPFVWVWVKKPVATNIPKPVVSVYVQVQVNSVQVWVWV 179  
 DB 1  
 QY 171 SDQWKPKVPPVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 180  
 DB 1  
 QY 180 ISKILFETVLSHAPKIVSVASAKISKSKSLDVKVHSTIKSLATOLQVHAN 219  
 DB 1  
 QY 181 ISKILFETVLSHAPKIVSVASAKISKSKSLDVKVHSTIKSLATOLQVHAN 240  
 DB 1  
 QY 246 KIPVNNWNNQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 296  
 DB 1  
 QY 291 KAPVNNWNNQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 299  
 DB 1  
 QY 359 PPSVSVDEIMTVLYPEYWKMKKQVFKKAWHNPSSSTPSPDSKFAAAHYNAATIK 418  
 DB 1  
 QY 360 PPSVSVDEIMTVLYPEYWKMKKQVFKKAWHNPSSSTPSPDSKFAAAHYNAATIK 419  
 DB 1  
 RESULT 10  
 AAY70982  
 ID AAY70982 standard; Protein: 419 AA.  
 XX  
 AC AAY70982;  
 XX  
 DI 09-AUG-2000 (first entry)  
 XX  
 DE Human vascular endothelial growth factor (VEGF)-C protein.  
 XX  
 KW Vascular endothelial growth factor-C; VEGF; human; re-endothelialisation;  
 KW vascular endothelial growth factor receptor; VEGFR; vascular trauma;  
 KW blood vessel; cardiovascular surgery; anti restenosis agent; prevention;  
 KW restenosis; stenosis; percutaneous transluminal coronary angioplasty.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..31  
 FT /Label= Signal peptide  
 FT /note= "Cleavage results in partially-processed VEGF-C  
 protein (29 kD)"  
 FT 32..103  
 FT /Label= Amino-terminal peptide  
 FT /note= "Cleavage results in fully-processed mature  
 VEGF-C protein (21-23 kD)"  
 FT 104..227  
 FT /Label= Mature\_human\_VEGF-C  
 FT /note= "Processed vascular epithelial growth factor-C"  
 FT 228..419  
 FT /Label= C-terminal peptide  
 FT /note= "Essential for VEGFR-2 and VEGFR-3 binding"  
 FT 131..211  
 FT /note= "Essential for biological activity of protein"  
 FT Binding-site 137  
 FT /note= "Essential for VEGFR-2 and VEGFR-3 binding"  
 FT Binding-site 156  
 FT /note= "Essential for VEGFR-2 binding"  
 FT Binding-site 165

[illegible]

RESULT 11  
 AAB47605 standard; protein; 419 AA.  
 XX  
 AC AAB47605;  
 XX  
 PE 27-FEB-2001 (first entry)  
 XX  
 DE Human VEGF-C.  
 XX  
 KW Human; gene therapy; lymphatic disorder; hereditary lymphedema; FHL4;  
 XX vascular endothelial growth factor receptor v; VEGFR-v; VEGP-C; VEGP-D;  
 XX fms-like tyrosine kinase 4.  
 XX  
 OS Homo sapiens.  
 XX  
 CA Z0470-A1.  
 EN  
 ID 26 SEP-2000.  
 XX  
 FE 29 SEP-1999; 99CA-2284470.  
 XX  
 PR 26 MAR-1999; 99MO-US06144.  
 XX  
 PL 16 APR-1999; 99US-037524H.  
 XX  
 PA (OYPR-) UNIV HETTSRUGH.  
 XX (OYPR-) UNIV HEELSTINK LIPENSTING LTD OF,  
 XX (LUDW) LIMBIG INST CANCER RES.  
 P1 Alltalo K., Portelli JE., Fitzgerald JN., Karakarnia M.  
 XX  
 WP1: 2001-067762/02.  
 DR N-PUBM; AAC68954.  
 XX  
 PT Screening a human for an increased risk of developing lymphatic  
 PS disorder comprises assaying nucleic acid for alterations in the  
 PP sequences expressing vascular endothelial growth factor receptor-4.  
 XX  
 DS Disclosure: Pages 62-63; 99pp; English.  
 XX  
 CE The present invention relates to a method for screening a human subject  
 CC for an increased risk of developing a lymphatic disorder e.g. hereditary  
 CC lymphedoma. The method comprises assaying nucleic acid of a human  
 CC subject to determine a presence or an absence of a mutation affecting the  
 CC sequence of expression of vascular endothelial growth factor receptor-4  
 CC (VEGFR-4)/fms like tyrosine kinase 4 (FLT4) allele (see AAC68954 and  
 CC AAC47604) and determining an increased risk of developing lymphatic  
 CC disorder from presence or absence of the mutation. The presence of a  
 CC mutation affecting the encoded amino acid sequence of expression of at  
 CC least 1 VEGFR-4 allele in the nucleic acid correlates with an increased  
 CC risk of developing a lymphatic disorder. Treatment for hereditary  
 CC lymphedoma can be provided through the administration of vascular  
 CC endothelial growth factor C (VEGF-C) and/or vascular endothelial growth  
 CC factor D VEGF-D genes (via gene therapy) and proteins. The present  
 CC sequence is the protein sequence for VEGF-C.  
 XX  
 SO Sequence 419 AA:

Query Match:	76..78;	Score 1804.5;	DB 22;	Length 419;
Host Local Similarity:	75..78;	Prod. No.	1-96-142;	
Matches	418;	Conservative	39;	Mismatches 60;
			Indels	4;
			Gaps	4;

```

MIHEEMLSATTAAGAVLLTPPGPPVAAAFPSBHYEFPGAEPKMAKSIALEPOL   59
IIII I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I
I mlllglsydslllaadlppmcpagdaadaaaesdlldsdapgaatdayaskdvecl 60

RSVSSEIEMLGVLYGYVMFMPLQPEKTLGWLNREHSISDILSKDSIKLAAMAYNAFLIK 119
IIIIIIIIIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
61 RSVSSEIEMLGVLYGYVMFMPLQPEKTLGWLNREHSISDILSKDSIKLAAMAYNAFLIK 120

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1F 10 MAR 1999: 99060 USP021.  
 XX  
 1K MAR 1998: 9805 0042105.  
 1R 01 JUN 1998: 9805 0107997.  
 1A (HUMA ) HUMAN GENOME SET INC.  
 XX  
 1I Boston CA, Cao L, Hu J:  
 1X WPL: 1999-44366/46.  
 1R N-PSDB: AAX8437.  
 1T New human vascular endothelial growth factor-2, used for treating, e.g.,  
 1X immune disorders and cancers.  
 1S Claim 1: Fig 1A-E: 22pp: English.  
 1X  
 1C The present sequence represents vascular endothelial growth factor-2  
 1C (VEGF-2). The VEGF-2 polypeptides have activating similar to VEGF. The  
 1C VEGF-2 polypeptides stimulate the growth of vascular endothelial cells,  
 1C stimulate endothelial cell migration, stimulate angiogenesis, decrease  
 1C blood pressure, and increase blood flow. The polypeptides and  
 1C polypeptides can be used for preventing, treating or ameliorating a  
 1C medical condition. The VEGF-2 polypeptides or polypeptides may be  
 1C useful in treating defective or disorders of the immune system, by  
 1C activation or inhibiting the proliferation, differentiation, or  
 1C modulation (chemotaxis) of immune cells. The etiology of these immune  
 1C deficiencies or disorders may be genetic, somatic, such as cancer or  
 1C some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or  
 1C infectious. Examples of immunologic deficiency syndromes include blood  
 1C protein disorders, ataxia telangiectasia, common variable  
 1C immunodeficiency, DiGeorge syndrome, HIV infection, HTLV-III infection,  
 1C leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte  
 1C bactericidal dysfunction, severe combined immunodeficiency (SCID),  
 1C Minkowski-Albright disorder, anemia, thrombocytopenia, or hemoglobinuria.  
 1C They can also be used to modulate constitutive or tumorigenic activity.  
 1C Stimulatory allergic reactions and conditions such as asthma (particularly  
 1C allergic asthma) or other respiratory problems, may also be treated.  
 1X  
 1X Sequence: 419 AA:  
 1X  
 1X Query Match: 76.2%; Score 1794.5; Dh 20; Length 419;  
 1X Best Local Similarity: 75.2%; Pred. No. 1, 6-141;  
 1X Matches: 316; Conservative: 40; Mismatches: 61; Indels: 3; Gaps: 3;

1X RES011\_14  
 1X AAY22320  
 1D AAY22320 standard: Protein: 419 AA.  
 1X  
 1X AC AAY22320:  
 1X  
 1X 22-SEP-1999 (first entry)  
 1X  
 1X Full length human VEGF2 protein sequence.  
 1X  
 1X VEGF2: vascular endothelial growth factor 2; angiogenesis; bone damage;  
 1X endothelial cell proliferation; tissue damage; therapy.  
 1X  
 1X Homo sapiens:  
 1X  
 1X OS9932540-A.  
 1X  
 1X 03-MAR-1999.  
 1X  
 1X 24-DEC-1997: 9705-099811.  
 1X  
 1X 24-DEC-1997: 9705-099811.  
 1X 08 MAR 1994: 9405-0207550.  
 1X 06-JUN-1995: 9505-0465968.  
 1X  
 1X (HUMA-) HUMAN GENOME SET INC.  
 1X  
 1X Cao L, Boston CA:  
 1X  
 1X WPL: 1999-44366/47.  
 1X N-PSDB: AAX8437.  
 1X  
 1X Vascular endothelial growth factor 2 for wound healing and vascular  
 1X repair.  
 1X  
 1X Claim 1: Fig 1: 4pp: English.  
 1X  
 1X This sequence is the vascular endothelial growth factor 2 (VEGF2).  
 1X of the invention. The isolated polypeptide is useful for stimulating  
 1X angiogenesis, by promoting the proliferation of endothelial cells, for  
 1X the treatment of a wound, or for the treatment of tissue or bone damage.  
 1X  
 1X Sequence: 419 AA:  
 1X  
 1X Query Match: 76.2%; Score 1794.5; Dh 20; Length 419;  
 1X Best Local Similarity: 75.2%; Pred. No. 1, 6-141;  
 1X Matches: 316; Conservative: 40; Mismatches: 61; Indels: 3; Gaps: 3;







GenPlot version 4.5  
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OM protein - protein search, using SW model

Run on:	February 20, 2002, 16:23:57	: Search time 43.31 Seconds
		(without alignments)
		1401.594 Million cell updates/sec

Title: US-09-534-376A-11  
 Port of entry: 3341

Sequence: I MHLICFISLACSLAAAI.P. . . . . SFSSEVVKVPSYWKPHLN 415

Scoring table:  $\text{ELUSIM62}$   
 $\text{Gapop } 10.0$  ,  $\text{Gapext } 0.5$

*See also*: 47300-5079; 47300-5080-5086; 47300-5087-5090; 47300-5091-5092; 47300-5093-5094; 47300-5095-5096; 47300-5097-5098; 47300-5099-5100; 47300-5101-5102; 47300-5103-5104; 47300-5105-5106; 47300-5107-5108; 47300-5109-5110; 47300-5111-5112; 47300-5113-5114; 47300-5115-5116; 47300-5117-5118; 47300-5119-5120; 47300-5121-5122; 47300-5123-5124; 47300-5125-5126; 47300-5127-5128; 47300-5129-5130; 47300-5131-5132; 47300-5133-5134; 47300-5135-5136; 47300-5137-5138; 47300-5139-5140; 47300-5141-5142; 47300-5143-5144; 47300-5145-5146; 47300-5147-5148; 47300-5149-5150; 47300-5151-5152; 47300-5153-5154; 47300-5155-5156; 47300-5157-5158; 47300-5159-5160; 47300-5161-5162; 47300-5163-5164; 47300-5165-5166; 47300-5167-5168; 47300-5169-5170; 47300-5171-5172; 47300-5173-5174; 47300-5175-5176; 47300-5177-5178; 47300-5179-5180; 47300-5181-5182; 47300-5183-5184; 47300-5185-5186; 47300-5187-5188; 47300-5189-5190; 47300-5191-5192; 47300-5193-5194; 47300-5195-5196; 47300-5197-5198; 47300-5199-5200; 47300-5201-5202; 47300-5203-5204; 47300-5205-5206; 47300-5207-5208; 47300-5209-5210; 47300-5211-5212; 47300-5213-5214; 47300-5215-5216; 47300-5217-5218; 47300-5219-5220; 47300-5221-5222; 47300-5223-5224; 47300-5225-5226; 47300-5227-5228; 47300-5229-5230; 47300-5231-5232; 47300-5233-5234; 47300-5235-5236; 47300-5237-5238; 47300-5239-5240; 47300-5241-5242; 47300-5243-5244; 47300-5245-5246; 47300-5247-5248; 47300-5249-5250; 47300-5251-5252; 47300-5253-5254; 47300-5255-5256; 47300-5257-5258; 47300-5259-5260; 47300-5261-5262; 47300-5263-5264; 47300-5265-5266; 47300-5267-5268; 47300-5269-5270; 47300-5271-5272; 47300-5273-5274; 47300-5275-5276; 47300-5277-5278; 47300-5279-5280; 47300-5281-5282; 47300-5283-5284; 47300-5285-5286; 47300-5287-5288; 47300-5289-5290; 47300-5291-5292; 47300-5293-5294; 47300-5295-5296; 47300-5297-5298; 47300-5299-5300; 47300-5301-5302; 47300-5303-5304; 47300-5305-5306; 47300-5307-5308; 47300-5309-5310; 47300-5311-5312; 47300-5313-5314; 47300-5315-5316; 47300-5317-5318; 47300-5319-5320; 47300-5321-5322; 47300-5323-5324; 47300-5325-5326; 47300-5327-5328; 47300-5329-5330; 47300-5331-5332; 47300-5333-5334; 47300-5335-5336; 47300-5337-5338; 47300-5339-5340; 47300-5341-5342; 47300-5343-5344; 47300-5345-5346; 47300-5347-5348; 47300-5349-5350; 47300-5351-5352; 47300-5353-5354; 47300-5355-5356; 47300-5357-5358; 47300-5359-5360; 47300-5361-5362; 47300-5363-5364; 47300-5365-5366; 47300-5367-5368; 47300-5369-5370; 47300-5371-5372; 47300-5373-5374; 47300-5375-5376; 47300-5377-5378; 47300-5379-5380; 47300-5381-5382; 47300-5383-5384; 47300-5385-5386; 47300-5387-5388; 47300-5389-5390; 47300-5391-5392; 47300-5393-5394; 47300-5395-5396; 47300-5397-5398; 47300-5399-5400; 47300-5401-5402; 47300-5403-5404; 47300-5405-5406; 47300-5407-5408; 47300-5409-5410; 47300-5411-5412; 47300-5413-5414; 47300-5415-5416; 47300-5417-5418; 47300-5419-5420; 47300-5421-5422; 47300-5423-5424; 47300-5425-5426; 47300-5427-5428; 47300-5429-5430; 47300-5431-5432; 47300-5433-5434; 47300-5435-5436; 47300-5437-5438; 47300-5439-5440; 47300-5441-5442; 47300-5443-5444; 47300-5445-5446; 47300-5447-5448; 47300-5449-5450; 47300-5451-5452; 47300-5453-5454; 47300-5455-5456; 47300-5457-5458; 47300-5459-5460; 47300-5461-5462; 47300-5463-5464; 47300-5465-5466; 47300-5467-5468; 47300-5469-5470; 47300-5471-5472; 47300-5473-5474; 47300-5475-5476; 47300-5477-5478; 47300-5479-5480; 47300-5481-5482; 47300-5483-5484; 47300-5485-5486; 47300-5487-5488; 47300-5489-5490; 47300-5491-5492; 47300-5493-5494; 47300-5495-5496; 47300-5497-5498; 47300-5499-5500; 47300-5501-5502; 47300-5503-5504; 47300-5505-5506; 47300-5507-5508; 47300-5509-5510; 47300-5511-5512; 47300-5513-5514; 47300-5515-5516; 47300-5517-5518; 47300-5519-5520; 47300-5521-5522; 47300-5523-5524; 47300-5525-5526; 47300-5527-5528; 47300-5529-5530; 47300-5531-5532; 47300-5533-5534; 47300-5535-5536; 47300-5537-5538; 47300-5539-5540; 47300-5541-5542; 47300-5543-5544; 47300-5545-5546; 47300-5547-5548; 47300-5549-5550; 47300-5551-5552; 47300-5553-5554; 47300-5555-5556; 47300-5557-5558; 47300-5559-5560; 47300-5561-5562; 47300-5563-5564; 47300-5565-

Total number of hits satisfying chosen parameters. 473505

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Minimum PB seq length: 0
Maximum PB seq length: 2000000000
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Post processing:	Minimum Match 0%
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	Listing first 45 summaries

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Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
	1	2017.5	87.9	479	4	Q9XSP0	Q9XSP0	Canis lupus
	2	1762.5	75.5	418	13	Q57332	Q57332	Columba livia
	3	696	29.8	354	4	Q43915	Q43915	Homo sapiens
	4	689.5	29.6	354	11	P67946	P67946	Mus musculus
	5	689	29.5	146	11	Q35757	Q35757	Rattus norvegicus
	6	658.5	28.2	326	11	Q35251	Q35251	Rattus norvegicus
	7	274.5	11.8	1744	5	Q94446	Q94446	Chloromys
	8	260	11.1	1648	5	Q94438	Q94438	Chloromys
	9	231	9.9	242	4	Q9H1W9	Q9H1W9	Homo sapiens
	10	231	9.9	244	4	Q9H689	Q9H689	Homo sapiens
	11	232.5	9.5	214	6	Q9MYV3	Q9MYV3	Homo sapiens
	12	211.5	9.5	208	6	Q9XSP4	Q9XSP4	Canis familiaris
	13	217.5	9.3	209	4	Q60720	Q60720	Homo sapiens
	14	217.5	9.3	214	5	Q9XSP5	Q9XSP5	Canis familiaris
	15	214.5	9.2	140	6	Q9XSP3	Q9XSP3	Canis familiaris
	16	212.5	9.1	140	6	Q9GK80	Q9GK80	Equus caballus
	17	208.5	8.9	130	6	Q9C152	Q9C152	Sus scrofa
	18	205	8.8	122	6	Q9C131	Q9C131	Bos taurus
	19	203	8.7	144	13	Q42272	Q42272	Xenopus laevis

20	199.5	8.6	190	6	077644	077644 ovis aries
21	199.5	8.6	190	11	090X39	090X39 staxix leont
22	199.5	8.6	191	4	076875	076875 homo sapien
23	196.5	8.4	214	11	090X67	090X67 rattus norv
24	195	8.4	174	4	090123	090123 homo sapien
25	190.5	8.2	190	11	090X51	090X51 muscoriceta
26	188.5	8.1	188	13	074682	074682 brachydonia
27	188.5	8.1	34	5	090181	090181 dirosophia
28	188.5	8.1	704	3	074567	074567 trichostema
29	187.5	8.0	171	4	090198	090198 homo sapien
30	184.5	7.9	147	4	090H58	090H58 homo sapien
31	184	7.9	142	11	090E16	090E16 muscoriceta
32	181.5	7.8	150	11	054881	054881 rattus norv
33	180	7.7	124	6	090K60	090K60 callithrix
34	180	7.7	301	5	090W66	090W66 dirosophia
35	179.5	7.7	148	13	042571	042571 xenopus lae
36	179.5	7.7	188	6	090S48	090S48 bos taurus
37	176.5	7.6	2352	5	061240	061240 halcyonithia
38	176	7.5	326	6	090D97	090D97 macaca mula
39	176	7.5	800	5	090H78	090H78 drosophila
40	172.5	7.4	118	6	090E31	090E31 ovis aries
41	172	7.4	2471	4	094721	094721 homo sapien
42	172	7.4	090240			090240 homo sapien
43	171.5	7.4	170	11	090J87	090J87 rattus norv
44	170	7.3	2471	11	090K80	090K80 rattus norv
45	169.5	7.3	146	11	090X06	090X06 rattus norv

## ALICOMMENTS

[illegible]

[illegible]

QY	61	RSSVSVLMSVLYTGYMKKQULPRKQW	QY11INTERPSSVFAAHNTEELK	119
		:       :       :       :		
Dbb	60	RSSVSVLMSVLYTGYMKKQULPRKQW	QY11INTERPSSVFAAHNTEELK	119
QY	117	SLINEMWVQMLHPVTLVWRPFAALNIPKQWVSVYRQVQVNSKPLQMLNLSQY		176
Dbb	120	SLTFEMKQULMRCVCVQVQCEVQALNIPKQWVSLYKQVQVNSKPLQMLNLSQY		179
QY	177	LSKIDPEETVPISSQGRVITVSPFNHISQWMSKLDVYQVQVNSLIRSLDNLDPQVQAN		246
		:       :       :       :       :       :       :		
Dbb	180	LSKIDPEETVPISSQGRVITVSPFNHISQWMSKLDVYQVQVNSLIRSLDNLDPQVQAN		249
QY	247	KICPTNYWNNIPKQULQULPQVSVNEDTSMNRPVQGRKHELDPEQVQKGL		295
		:       :       :       :       :       :       :		
Dbb	240	KICPTNYWNNIPKQULQULPQVSVNEDTSMNRPVQGRKHELDPEQVQKGL		298
QY	266	RSSVQGRKHELDQVQVCKKKQLPNSCANDEPEENIQVQVCKRQVPRQVLPNPKCA		355
		:       :       :       :       :       :       :		
Dbb	269	RSSVQGRKHELDQVQVCKKKQLPNSCANDEPEENIQVQVCKRQVPRQVLPNPKCA		358
QY	456	QY11ENIQVQVCKKQKHLQVSVYPRQVANKRQVQVGLSLSEVQVQVPSWNRQHLN		415
		:       :       :       :       :       :       :		
Dbb	459	QY11ENIQVQVCKKQKHLQVSVYPRQVANKRQVQVGLSLSEVQVQVPSWNRQHLN		418

[illegible]

Genotype	Method	Stomach	Small Int.	Large Int.	Caeca
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3	3	3	3	3	3
4	4	4	4	4	4
5	5	5	5	5	5
6	6	6	6	6	6
7	7	7	7	7	7
8	8	8	8	8	8
9	9	9	9	9	9
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71	71	71	71	71	71
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75	75	75	75	75	75

RESULT	4			
LD	04/915	PRELIMINARY:	PERT:	854 AA.
AC	04/915			
DT	01-JUN-1998 (TERMINAL: 06, (Treated))			
DT	01-JUN-1998 (TERMINAL: 06, (last sequence update))			
DT	01-JUN-2001 (TERMINAL: 17, (last annotation update))			
DE	GROWTH FACTOR FIGF.			
GN	FIGF OR VEGF-B.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eulipotyria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxId:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	ME0101:98143120; PubMed 9474494;			
RA	Rochelandi M., Testini M., Lodi A., of Landini M., Frasco B.,			
RA	Rossi F., Ballabio A., Zuffardi O., Oliverio S.;			
RT	"Human FIGF: cloning, gene structure, and mapping to chromosome Xp22,			
RT	between the FIGA and the GDF genes.";			
RL	Genomics 47:207-216(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE: LUNG;			
RX	ME0101:97349118; PubMed 9205122;			
RA	Yamada Y., Nezu J., Shimizu M., Hirata Y.;			
RT	"Molecular cloning of a novel vascular endothelial growth factor,			
RT	VEGF-1.";			
RL	Genomics 42:484-488(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	ME0101:98118549; PubMed 9435229;			
RA	Achen M.G., Jeltsch M., Kikk E., Mäkinen T., Vitali A., Wilks A.F.,			
RA	Allitalo K., Stacker S.A.;			
RT	"Vascular endothelial growth factor-1 (VEGF-1) is a ligand for the			
RT	tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt1).";			
RL	Proc. Natl. Acad. Sci. U.S.A. 95:548-554(1998).			
DR	EMBL: Y12864; CAAT3371.1; JOINED.			
DR	EMBL: Y12865; CAAT3371.1; JOINED.			
DR	EMBL: Y12866; CAAT3371.1; JOINED.			
DR	EMBL: Y12867; CAAT3371.1; JOINED.			
DR	EMBL: Y12868; CAAT3371.1; JOINED.			
DR	EMBL: Y12869; CAAT3371.1; JOINED.			
DR	EMBL: Y12870; CAAT3371.1; JOINED.			
DR	EMBL: D89540; BAA24264.1; -.			
DR	EMBL: AF060185; CAA04942.1; -.			
DR	EMBL: Y12864; CAAT3370.1; -.			
DR	HSSNY: F15692; IVP.			











Search completed: February 20, 2002, 16:27:08  
Job time: 191 sec



GenTools version 4.5  
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protein - protein search, using sw model

Perfect score: 233  
Sequence: 1 MHLTFLSIACSLTAALP.....SPSEEVQRCVPYWKRPILN 415

Scoring table: `BL0SUM62`  
`Gapop 10.0` , `Gapext 0.5`

Searched: 100059 seqs, 46564827 residues  
Total number of hits satisfying chosen parameters

```
Minimum PB seq length: 0
Maximum PB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
Maximum Match 100%
listing first 45 summaries
```

Fixed. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARY

Result	No.	Score	Quality	Match	Length	PR	ID	Descrptd Loc
	1	2333	100.0	415			VEGG_MOUSE	P47963 mus musculus
	2	2344	87.8	413			VEGG_HUMAN	E47967 homo sapiens
	4	271.5	11.6	1700			BAR3_CHITE	G03376 Chironomus
	4	213.5	9.2	215			VEGG_HUMAN	F15632 homo sapiens
	5	211.5	9.1	190			VEGG_PIG	P49351 sus scrofa
	6	201.5	8.6	193			VEGG_PAT	P165512 Rattus norvegicus
	7	198.5	8.5	190			VEGG_HOVIN	P15641 bos taurus
	8	195.5	8.4	164			VEGG_GAVPO	P266172 cavia porcellus
	9	195.5	8.4	214			VEGG_MOUSE	G06741 mus musculus
	10	190.5	8.2	474			FP2_MYTA	G25454 Mytilus gal
	11	179.5	7.7	188			VEGG_MOUSE	P49766 mus musculus
	12	178.5	7.7	186			VEGG_HUMAN	P49765 homo sapiens
	13	173.5	7.4	146			VEGG_SHEEP	P50412 ovis aries
	14	173	7.4	216			VEGG_CHICK	F25582 Gallus gallus
	15	163	7.0	2703			NOTO_DROME	P072872 Drosophila
	16	162.5	7.0	134			VEGG_DROME	F05841 Gtf vitreus
	17	161.5	6.9	1664			NTCA_MOUSE	F10755 mus musculus
	18	160	6.9	148			VEGG_MOUSE	F52855 Gtf vitreus
	19	159.5	6.8	3535			IMAG_MOUSE	G61001 mus musculus
	20	155.5	6.7	2482			WVE_FIG	G28833 Sus scrofa
	21	155	6.6	2444			NOTO_HUMAN	F46541 homo sapiens
	22	152.5	6.5	170			PEGE_HUMAN	P49743 homo sapiens
	23	151.5	6.5	2437			NOTO_PXAVE	P46500 brachydanio
	24	151.5	6.5	2871			NOTO_HUMAN	F55555 homo sapiens
	25	151	6.5	3672			IML2_CARTEL	G21373 Caenorhabditis
	26	149	6.4	1557			IML1_CARTEL	G01883 Caenorhabditis
	27	148	6.3	2139			GRB_DROME	P10040 Drosophila
	28	148	6.3	2813			WVF_GAVPA	G282455 canis familiaris
	29	147.5	6.3	2524			NOTO_XENLA	F21783 xenopus laevis
	30	147.5	6.3	2524			NIQI_MOUSE	G01705 mus musculus
	31	147.5	6.3	2871			FRNI_HOVIN	P04173 bos taurus
	32	147	6.3	2871			FRNI_PIG	P04173 bos taurus
	33	146.5	6.3	1790			LRB_DROME	P11045 Drosophila

34	146	6.3	287.1	1	FBM1_MOUSE	Q61554	mus musculus
35	145.5	6.2	798	1	ITB1_XENLA	P12606	xenopus laevis
36	145.5	6.2	14.9	1	L12_CAEEL	P43565	caenorhabditis elegans
37	145.5	6.2	2957	1	FBM2_MOUSE	P45556	mus musculus
38	145.5	6.2	2911	1	FBM2_HUMAN	P45556	homo sapiens
39	145	6.2	1680	1	FBP2_DROME	P30432	drosophila melanogaster
40	144.5	6.2	1040	1	FBP1_STRIO	P10079	striatum loricatum
41	144	6.2	798	1	ITB1_HUMAN	P05556	homo sapiens
42	142.5	6.1	1746	1	TEMA_FIG	G93116	sus scrofa
43	142.5	6.1	25.1	1	ITC1_RAI	G07009	rattus norvegicus
44	141	6.0	1808	1	TEMA_CHICK	P10079	rattus norvegicus
45	141	6.0	2813	1	VWF_HUMAN	P04275	homo sapiens

## AI, COMMENTS

VEGC_MOUSE	STANDARD:	PRT:	415 AA.
AC	15-JUL-1998 (Ref. 36, Created)		
DT	15-JUL-1998 (Ref. 36, Last sequence update)		
DT	20-AUG-2001 (Ref. 40, Last annotation update)		
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (FLT4 LIGAND) (FLT4-L).		
GN	VbGfC.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BA1B/C;		
RX	MEDLINE=97164697; PubMed=9012504;		
RA	Kirk E., Lydenassaki A., Taira S., Kaipainen A., Jeltsch M.,		
RA	Jonkov V., Alladio K.;		
RT	"VEGF-C receptor binding and pattern of expression with VEGFR-3		
RL	suggests a role in lymphatic and vascular development.";		
RL	Development 122:3825-3837(1996).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BA1B/C;		
RX	MEDLINE=97388452; PubMed=9247716;		
RA	Fitz L.J., Morris I.C., Towler P., Long A., Burgess P., Gervo K.,		
RA	Wang L., Gassaway K., Nickbarg E., Kovacic S., Charletta A.,		
RA	Gianotti J., Minorty H., Zollner P., Behar D.P., Long L.V.,		
RA	Turner K.J., Wood C.K.;		
RT	"Characterization of murine Flt4 ligand/VEGF-C.";		
RL	Oncogene 15:611-618(1997).		
CC	-1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHelial		
CC	CELL GROWTH.		
CC	-1- SIMILARITY: HOMODIMERS; DISULFIDE-LINKED (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO THE VEGF/VEGF FAMILY OF GROWTH FACTORS.		
CC	-----		
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CC	OR SEND AN EMAIL TO <a href="mailto:license@isb.slb.ch">license@isb.slb.ch</a> ).		
CC	-----		
DR	EMBL: U71620; AAC52984.1; -		
DR	EMBL: U58112; AAB46707.1; -		
DR	BSP: P15692; IVP.		
DR	MED: M61109124; VEGfC.		
DR	TrEMBL: IPR002400; GF_VEGfC.		
DR	TrEMBL: IPR000072; PDGF.		
DR	PIR: PR00441; PDGF; 1		
DR	PRINTS: PR00438; GPCYSKNOT.		
DR	Protein: PR001629; PDGF; 1.		
DR	SMART: SM00141; PDGF; 1.		













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CX      NBI_TaxID=10090:
RP      SEQUENCE FROM N.A.
RX      MEDLINE=92274860; PubMed=1592003; Risan W.;
RA      Breit G., Albrecht U., Sterrer S.,
RT      "Expression of vascular endothelial growth factor during embryonic
RN      angiogenesis and endothelial cell differentiation."
RL      development 114:521-532(1992).
RP      SEQUENCE FROM N.A. (VEGF-1).
RX      MEDLINE=92355593; PubMed=1644816;
RA      Claffey K.P., Wilkison W.O., Spiegelman B.M.;
RT      "Vascular endothelial growth factor. Regulation by cell
RN      differentiation and activated second messenger pathways."
RL      J. Biol. Chem. 267:16317-16322(1992).
RP      [3]
RN      SEQUENCE OF 1-3 FROM N.A.
RX      MEDLINE=96216498; PubMed=8632007;
RA      Shima D.T., Kuroki M., Deutsch U., Ng Y., Adams A.P., D'Amore P.A.;
RT      "The mouse gene for vascular endothelial growth factor. Genomic
RN      structure, definition of the transcriptional unit, and
RT      characterization of transcriptional and post-transcriptional
RL      regulatory sequences."
RJ      J. Biol. Chem. 271:3877-3883(1996).
CC      -1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS AND ENDOTHELIAL
CC      CELL GROWTH INDICES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC      PERMEABILITY.
CC      -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC      -1- SUBCELLULAR LOCATION: VEGF 1 AND VEGF-2 ARE SECRETED WHILE
CC      VEGF-3 REMAINS CELL-SURFACE ASSOCIATED UNLESS RELEASED BY
CC      HEPARIN.
CC      -1- ALTERNATIVE PRODUCTS: THREE FORMS (VEGF-1, VEGF-2 AND VEGF-3) ARE
CC      PRODUCED AS A RESULT OF ALTERNATIVE SPLICING OF THE SAME GENE. THE
CC      LONGEST FORM (VEGF-3, SHOWN HERE) CONTAINS A BASIC INSERT LINKED
CC      TO CELL-ASSOCIATION/HEPARIN-BINDING.
CC      -1- TISSUE SPECIFICITY: IN DEVELOPING EMBRYOS, EXPRESSED MAINLY IN
CC      THE CHOROID PLEXUS, PAVEMENTAL NEUROEPITHELIUM, PLACENTA AND
CC      KIDNEY GLOMERULI. ALSO FOUND IN BRONCHIAL EPITHELIUM, ADIPONAL
CC      GLAND AND IN SEMINIFEROUS TUBULES OF TESTIS. HIGH EXPRESSION OF
CC      VEGF CONTINUES IN KIDNEY GLOMERULI AND CHOROID PLEXUS IN ADULTS.
CC      -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC
CC      -----
CC      THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION
CC      BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION -
CC      THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS
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CC      ENTITIES REQUIRES A LICENSE AGREEMENT (SEE http://www.isb-sib.ch/announce/
CC      OR SEND AN EMAIL TO license@isb-sib.ch).
CC      -----
DR      EMBL: S37052; AAB32352.1; -
DR      EMBL: S38083; AAB22253.1; -
DR      EMBL: S34109; AAB22254.1; -
DR      EMBL: M95200; AAA40547.1; -
DR      EMBL: U41833; - NOT_ANNOTATED_CDS.
DR      PIR: A43351; A43351.
DR      HSSP: P15692; ZVGH.
DR      MGD: MGI:103178; Vegf.
DR      InterPro: IPR000072; PDGF.
DR      Pfam: PF00341; PDGF; 1.
DR      ProDom: PD001629; PDGF; 1.
DR      SMART: SM00141; PDGF; 1.
DR      PROSITE: PS00249; PDGF_1; 1.
DR      PROSITE: PS50276; PDGF_2; 1.
KW      Mitogen; growth factor; glycoprotein; Alternative splicing; Signal.
FT      SIGNAL: 1
FT      CHAIN: 27 214
FT      DISULFID 51 93
FT      DISULFID 82 127
FT      DISULFID 86 129
FT      DISULFID 76 76
FT      DISULFID 85 85
FT      DISULFID 100 100
FT      CAPROHYD
N-LINKED (GLCNAC. . .) (PROBALE).

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07 164 NSBGLQMNISLSTSLLEPLVLSG-----GKPLV-----ISFANHLCKMSKL 211
08 165 KNSHLEFENCKDYKCPVWVYSLDQENAKFENLNSMDLQSAKPOLVYSEPLP----- 229
09 212 IVYVWVNSHLEPSPVATLPGV-----AANFCTPTNYVNN-----MCPPLAAGCTIFYS 262
10 221 -----PGRPPPTPTVYAPPPKNNATSSNSGNGP----- 256
11 263 NVEHDSINSH -----PANNKLEDEPT-----QVCGKSLPSSNG----- 301
12 267 KQVSGFCAVWAKITLNNSSKLVHNGSYRLCKGQVSGHGLNCKENP 310
13 402 -----PKRLDPSGVV-----TNNLFNSAANFPTNTGVVFGTSPN 346
14 411 QNNKQVYPSNSDAEPKGVVQVTKQVCTPK-----PNN-----NINCKNKGDCNPN 360
15 447 QPLNGKCA-----ETP-----NTCKFLKCKK-----HNOT 376
16 361 GKTTCAVWCPKPTTKAVYKPPVVSCKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPK 420
17 377 GCGYR-----KPCANIKKHPDGLSPSEVCGCPVSY 408
18 421 KSKYKKNPCASPKCKNCKTKCKNY-----VCKCAPV 456

RESULT 11
VEGB_MOUSE STANDARD PRI 188 AA.
AC P49766:
DT 01-OCT-1996 (Rel. 34, Created)
DI 01-OCT-1996 (Rel. 34, Last sequence update)
DI 20-AUG-2001 (Rel. 40, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGB-B) (VASCULAR
ENOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRF).
GN VEGFB OR VRF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxonomy:10090:
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE: Heart;
RA MEDLINE-96197355; PubMed-8637916;
RA "Characterization of the murine VEGF-related factor gene.";
RA Ohtsuka H., Palusela K., Katsuragi A., von Euler G., Jonkov V.,
Saksela O., Orpana A., Pettersson R.P., Alitalo K., Pajksson U.;
RT "Vascular endothelial growth factor B, a novel growth factor for
endothelial cells.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:2576-2581(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE: Heart;
RA MEDLINE-9619052; PubMed 8607868;
RA Johnson S., Latorant J., Grimond S., Sillis G.,
Nordenskiold M., Weber G., Hayward N.K.;
RT "Characterization of the murine VEGF-related factor gene.";
RA Hoshino, Hoshino, K., Common, 220:922-928(1996).
CC -1- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
CC -1- SHUNT: HOMODIMER. DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER
WITH VEGF.
CC -1- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.
CC -1- TISSUE SPECIFICITY: AMNIOANTLY EXPRESSED IN HEART, BRAIN, KIDNEY
AND SKELETAL MUSCLE.
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS
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CC 00
DR EMBL: 048800; AAB06274.1; -
DR EMBL: 043837; AAC52553.1; -
DR HSSP: P15492; VEGF.
DR MGI: 106199; Vgfb.
DR InterPro: IPR003072; PDGF.
DR Pfam: PF00341; PDGF_1.
DR ProDom: ProDom629; PDGF_1.
DR SMART: SM00141; PDGF_1.
DR PROSITE: PS00249; PDGF_1;
DR PROSITE: PS0278; PDGF_2; 1.
KW Mitogenic growth factor; signal; heparin-binding;
FT SIGNAL 1 21
FT CHAIN 2 188
SQ SEQUENCE 188 AA; 21442 MW; 052A055FB945EYCA CRC64;
Query Match 7.7%; Score 179.5; DR 1; Length 188;
Best local Similarity 27.1%; Pred. No. 1.5e-07;
Matches 52; Conservative 24; Mismatches 77; Indels 39; Gaps 7;
07 104 KFAAHNTFLKSIDNEMKRTQMPREVCTDWSKEFGAATNPFKPPCVSVYKGGGCGN 163
08 25 QPSPHPGVVWPIFYAAVAT-QPSPVWPI SMPLMNVWQIVPS-VTVPGCGGCP 83
09 164 SEGLQMNISLSTSLLEPLVLSGPKVLLSFANHLCKMSKLVYQVSHLIR 223
10 84 PSHFQVPLDQVWVWQILMQLVPSNDR-----MSLEHSCVCPK-----KKSAAVAP 135
11 224 SEFATL-FOCOAN-----KTCPTNYVNNVWMCNCLAOQDFITYSVHDESTGFLDVG 277
12 16 NSPRTCTPTPTQPKPPTPTPTC-----PCKPPTP-----FLHGS 171
13 278 FNKLDEHTCC 289
14 172 KGLELNPVPC 183

RESULT 12
VEGB_HUMAN STANDARD PRI 188 AA.
AC P49765:
DT 01-OCT-1996 (Rel. 34, Created)
DI 01-OCT-1996 (Rel. 34, Last sequence update)
DI 20-AUG-2001 (Rel. 40, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGB-B) (VEGF PRELIMED
FACTOR).
GN VEGFB OR VRF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxonomy:9606:
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-96197355; PubMed-8637916;
RA Ohtsuka H., Palusela K., Katsuragi A., von Euler G., Jonkov V.,
Saksela O., Orpana A., Pettersson R.P., Alitalo K., Pajksson U.;
RT "Vascular endothelial growth factor B, a novel growth factor for
endothelial cells.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:2576-2581(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE-9707124; PubMed-891691;
RA Johnson S., Latorant J., Drinkwater G., Sillis G., Johnson S.,
Grimond S., Latorant J., Drinkwater G., Sakai S., Nordenskiold M., Ward L.,
Hayward N., Weber G.;
RT "Cloning and characterization of a novel human gene related to
vascular endothelial growth factor.";
RA Genome Res. 6:124-131(1996).
CC -1- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
CC -1- SHUNT: HOMODIMER. DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER
WITH VEGF.
CC -1- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR

```



RP SEQUENCE FROM N.A.  
 KC SPECIES: C. japonica; Tissue: Embryo;  
 RX MEDLINE: 96005007; PubMed: 7556923;  
 RA Flame 1; von Reuber M., Preker R.H., Syed-Ali S., Risan W.;  
 FT overexpression of vascular endothelial growth factor in the avian  
 R1 embryo induces hypervascularization and increased vascular  
 R1 permeability without alterations of embryonic pattern formation.\*;  
 R1 Dev. Biol. 171:439-444(1995).  
 RN [3]  
 RP SEQUENCE OF 60-187 FROM N.A.  
 KC SPECIES: C. japonica;  
 RA MEDLINE: 95491109; PubMed: 7781909;  
 RX Flame 1; Breier G., Risau W.;  
 R1 Vascular endothelial growth factor (VEGF) and VEGF receptor 2  
 R1 (11k-1) are expressed during vasculogenesis and vascular  
 R1 differentiation in the chick embryo.\*;  
 R1 Dev. Biol. 169:699-712(1995).  
 KC -1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL  
 CC CELL GROWTH, INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR  
 CC PERMEABILITY.  
 CC -1- SHORIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).  
 CC -1- ALTERNATIVE PRODUCTS: THREE ISOFORMS (VEGF-190, VEGF-146 AND VEGF-  
 CC 166) ARE PRODUCED AS A RESULT OF ALTERNATIVE SPLICING OF THE SAME  
 CC GENE. THE LONGER FORM CONTAINS A BASIC INSERT WHICH ACTS AS A CELL  
 CC RETENTION SIGNAL.  
 CC -1- TISSUE SPECIFICITY: ABUNDANTLY AND EQUALLY EXPRESSED IN HEART AND  
 CC LIVER, IN KIDNEY COMPEHENT, BRAIN AND YOLK SAC. VEGF-166 FORM IS  
 CC 5- TO 10- TIMES MORE ABUNDANT THAN THE VEGF-190 FORM.  
 CC -1- DEVELOPMENTAL STAGE: THE VEGF 166 FORM IS EXPRESSED EARLY AT DAY 1  
 CC AND IS UPGRADED DURING GASTRULATION. EXPRESSION OF THE VEGF-190  
 CC FORM IS DETECTABLE ONLY FROM DAY 2.  
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
 CC  
 CC This SWISS-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL collaboration  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 R6 EMBL: A001078; BAA24925.1;  
 R6 EMBL: S79680; AAR5371.1;  
 R6 HSRP: P15692; ZVGH.  
 DR InterPro: IP000072; Pfam:  
 DR Pfam: PF00441; Pfam: 1;  
 DR ProDom: P0001629; Pfam: 1;  
 DR SMART: SM00411; Pfam: 1;  
 DR PROSITE: PS00249; Pfam: 1;  
 DR PROSITE: PS0278; Pfam: 2; 1;  
 KW Mitogen; growth factor; glycoprotein; Alternative splicing; signal;  
 ET SIGNAL 1 26  
 ET CLAIN 27 216  
 ET DISULFID 84 128  
 ET DISULFID 87 130  
 ET DISULFID 77 72  
 ET DISULFID 86 86  
 ET CATHYD 101 101  
 ET VASAPLIC 142 142  
 ET VASAPLIC 143 166  
 ET VASAPLIC 166 166  
 ET VASAPLIC 167 210  
 ET SEQUENCE 216 AA; 26201 MW; 92966029 FCYGVY GYGG.  
 Query Match 7.48; Score 174; Dh 1; Length 216;  
 best local similarity 22.18; Pred. No. 5.7e-07;  
 Matches 46; Conservative 38; Mismatches 82; Indels 42; Gaps 8;  
 113 EELSTNEMKTKMPKPTIVTKPFAATNPKPPVSVVPPGCGGNSGGLQVYMC 172  
 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1  
 49 EVKTFE-VTKRSKRIFFTVVHPVPPVYVPPSVVIMMAGGQVGHLEIVY 97

QY 173 STGLSTLFFETVPLS QGKPVITSPANTSTGCKMLDYVQVNSTHRSPLA 227  
 Db 98 D-----VYVNMELARKPKHSCHLHMSPLHSGKQVKKVKNKQKRSRQKOR 150  
 QY 228 LHPQVANKLQCTENVMNMYKRCGLAQGLGVYVNLVLSINLHVGNKFLPRT 286  
 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1  
 Db 151 GQKKKKKKKKYKRP-----SPPKPPSPKPKHFLVY-----DQVT 185  
 QY 287 GQVCKGSLKPPSGGPKR-ELHDSGQC 413  
 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1  
 Db 186 GQSGCK-ELHSGKSGLELNEETPC 211  
 RESULT 15  
 NOTCDROME STANDARD; PRT: 2703 AA.  
 ID NOTCDROME STANDARD; PRT: 2703 AA.  
 AC P07207; P04154;  
 DT 01-NOV-1986 (Ref. 03; Created)  
 DE 01-FEB-1996 (Ref. 33; Last sequence update)  
 DT 20-APR-2001 (Ref. 40; Last annotation update)  
 DE NEUROGENIC LOCUS NOTCH PROTEIN PRECURSOR.  
 GN N.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscivora;  
 CC Ephydroidea; Drosophilidae; Drosophila.  
 CC MBI\_TaxID: 7227;  
 CX [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE: 860792535; PubMed: 3345325;  
 RA Warton K.A., Johnson K.M., Xu T., Aravanis-Tsakonas S.;  
 RT "A novel family of transcribed repeats shared by the Notch locus  
 RT and other developmentally regulated loci in D. melanogaster.\*";  
 RL Mol. Cell. Biol. 6:3094-3108(1986).  
 RN [3]  
 RP SEQUENCE OF 2505-2611 FROM N.A.  
 RX MEDLINE: 85094329; PubMed: 2981631;  
 RA Warton K.A., Johnson K.M., Johnson K.M., Xu T., Aravanis-Tsakonas S.;  
 RT "A novel family of transcribed repeats shared by the Notch locus  
 RT and other developmentally regulated loci in D. melanogaster.\*";  
 RL Mol. Cell. Biol. 6:3094-3108(1986).  
 RN [4]  
 RP SEQUENCE OF 1-8 FROM N.A.  
 RP MEDLINE: 8725944; PubMed: 3073327;  
 RA Kelley M.R., Kidd S., Berg R.L., Young M.W.;  
 RT "Restriction of P-element insertions at the Notch locus of Drosophila  
 RT melanogaster.\*";  
 RL Mol. Cell. Biol. 7:1545-1548(1987).  
 RN [5]  
 RP REVIEW.  
 RA Harris W.A.;  
 RT "Many cell types specified by Notch function.\*";  
 RL Curr. Biol. 1:120-122(1991).  
 CC 1. FUNCTION: NOTCH PROTEIN IS ESSENTIAL FOR PROPER DIFFERENTIATION OF  
 CC ECTODERM.  
 CC -1- STRUCTURAL LOCATION: TYPE 1 MEMBRANE PROTEIN.  
 CC -1- MISCELLANEOUS: SEPARATION OF NEUROBLASTS FROM THE ECTODERM INTO  
 CC THE INNER PART OF EMBRYO IS ONE OF THE FIRST STEPS OF CNS  
 CC DEVELOPMENT IN INSECTS. THIS PROCESS IS UNDER CONTROL OF THE  
 CC NEUROGENIC GENES.  
 CC -1- SIMILARITY: HIGH WITH OTHER NOTCH-TYPE PROTEINS.  
 CC -1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.  
 CC -1- SIMILARITY: CONTAINS 6 ANK REPEATS.



[illegible]

Search completed: February 20, 2002, 16:27:32  
Job time: 170 sec





Genome version 4.5  
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OM protein - protein search, using SW model

Run on: February 20, 2002, 16:20:52, Search time 27.95 seconds  
(without alignments)  
1229 978 Million cell updates/sec

Title: us-09-534-376a-11

Percent score: 2434

Sequence: 1 MHLGFLSLAGSLAAALIP.....SPSERVGVSTWKPPLN 415

Scoring table: BL/STMP62

Gapop: 10.0, Gapext: 0.5

Searched: 219241 seqs, 76174562 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 0%

Listing first 45 summaries

Database:

1: PIR-68:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR4:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2048	87.8	419	2 S69207	vascular endothel
2	271.5	11.6	1393	2 S08167	balb/c rat 3 pr
3	241	9.9	232	2 A41551	vascular endothel
4	211.5	9.1	190	2 S52130	vascular endothel
5	201.5	8.6	190	2 A35087	glioma-derived vas
6	200.5	8.6	190	2 B44881	vascular endothel
7	198.5	8.5	190	2 B40080	vascular endothel
8	195.5	8.4	214	2 A41981	vascular endothel
9	190.5	8.2	473	2 A56175	adhesive plaque pr
10	181	7.8	160	2 J06042	185k secretory pro
11	179.5	7.7	188	2 J06480	vascular endothel
12	176.5	7.6	233	2 J06291	rat heart-1 cell
13	173.5	7.4	146	2 S57956	ovine vascular end
14	172.5	7.4	139	2 A33787	vascular endothel
15	170	7.3	247	2 A4128	cell-tate detorma
16	167	7.2	1204	2 A43175	notch B protein -
17	164	7.0	2704	2 A44420	notch protein - fr
18	161.5	6.9	1964	2 T09059	16k vascular endo
19	160	6.9	148	2 D49630	vascular endothel
20	159.5	6.8	144	2 B49630	vascular endothel
21	159.5	6.8	3645	2 T10053	laminin alpha 5 ch
22	157	6.7	1372	2 T25933	hypothetical prote
23	154.5	6.6	149	2 A41236	placental growth f
24	154.5	6.6	2555	2 A49043	transmembrane prot
25	151.5	6.5	2432	2 S42632	fibillin-1 precu
26	151.5	6.5	3832	2 A47231	hypothetical prote
27	151	6.5	3672	2 T23433	probable laminin a
28	151	6.5	3704	2 T37416	hypothetical prote
29	150.5	6.5	545	2 T14108	

#### ALIGNMENTS

##### RESULT 1

S69207

vascular endothelial growth factor C precursor - human

MA:Alternate names: FLT4 ligand bHM

C:Species: Homo sapiens (man)

C:Date: 27-Apr-1996 #sequence, revision 01-Nov-1996 #text, change 08-Oct-1999

C:Accession: S69207, #sequence, S71443; S69208, #c2659

R:Joukov, V.; Pajusola, K.; Kaipainen, A.; Chlilov, D.; Lahninen, L.; Kukk, E.; Saksela

EMBO J. 15, 1751, 1996

A>Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand

A:Reference number: S69207; MIM:602004

A:Accession: S69207

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-419 <300>

A:Cross references: EMBL:X64216; NID-01172488; PIRN:CAAC3907.1; PIR:Q221096; PIR:Q118

A>Note: the nucleotide sequence was submitted to the EMBL data library, December 1996

A>Note: only a part of the translation is shown

A>Note: this is a revision to the sequence from reference S61795

R:Joukov, V.; Pajusola, K.; Kaipainen, A.; Chlilov, D.; Lahninen, L.; Kukk, E.; Saksela

EMBO J. 15, 290-298, 1996

A>Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the FLT4

A:Reference number: S61795; MIM:6018224

A:Accession: S61795

A:Status: nucleic acid sequence not shown, not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 70-419 <300>

A>Note: this sequence has been revised in reference S69207

A:Accession: S71443

A:Molecule type: protein

A:Residues: X, 124-120 <300>

R:Lee, J.; Gray, A.; Yuan, J.; Inoh, S.M.; Avraham, H.; Wood, W.L.

submitted to the EMBL data library, December 1995

A:Description: Vascular endothelial growth factor related protein (VRP): A ligand and

A:Accession number: S69208

A:Molecule type: mRNA

A:Residues: 1-419 <300>

A:Cross references: EMBL:044442; NID-01150988; PIRN:AA85214.1; PIR:Q1150989

R:Morris, J.C.

submitted to the EMBL data library, May 1996

A:Reference number: H01557

A:Accession: G02659

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-419 <300>

A:Cross references: EMBL:050111; NID-01373426; PIRN:AA02997.1; PIR:Q1374427

C:Gene: GDB:VEGFC; VRP

A:Cross references: GDB:3890883; OMIM:601528

F1 (2/Domain) Signal sequence #status predicted -SIG-

F1 (1/2/Domain) FGF-like #status predicted -pro-









104 KFAAAHYNLEELKSLINRMRKTCGMKCVLTWKEKGAALNTEKPPCVSVKGGGNN 164  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 25 GTHGSHGKKVYVWLVVAPATVAPRVVVLSEMLKSNVKGELVSSVTVVGRGGRCP 83  
 164 SDAAGMNTSTGYLSKSLPELVVPLSGDQKPVLSFANHTS\*PCMSKIDVYGVHSTLR 224  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 84 DMLDGVVLDQVEMQILMTQYSNGIDE \*MSLEFHSQVCHDK \* \* \* \* \* KLSAVNP 135  
 224 SLFATLTPGVANR KTCGVYVNRNRNRRRRLACGCTTYSVNRNRRNRRNRRN 277  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 146 DSRRLTTPVTDKQKRRRRR \* \* \* \* \* RRRRRR \* \* \* \* \* FLAQGG 171  
 278 PKELEDDPVGR 289  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 172 KGLRNLDPGRK 184  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 RESULT 12  
 140201  
 Match homolog protein - sea squirt (Haliorythia torvizi)  
 C/Spectrum: Haliorythia torvizi  
 C/Date: 02 Sep 2000 #sequence\_revision 02 Sep 2000 #tox\_change 02 Sep 2000  
 C/Accession: T40201  
 Roberty, S.; Saitoh, T.; Matsumoto, M.; Makabe, K.W.; Nishida, H.  
 Dev. Genes Evol. 267: 371-380, 1997  
 Article: Notch homologous from Haliorythia torvizi is preferentially expressed in the con-  
 A/Reference number: 267776  
 A/Accession: T40201  
 A/Status: preliminary  
 A/Molecule type: translated from cDNA  
 A/Residues: 1-2652  
 A/Cross-References: EMBL:AA001427; NID:012044722; PDB:0126501; PDB:0AA25571.1  
 C/Keyword: Notch  
 Query Match 7.48; Score 176.5; DB 2; Length 2452;  
 Best Local Similarity 20.98; Prod. No. 5; To 0;  
 Matches 102; Conservative 47; Mismatches 174; Indels 165; Gaps 26;  
 44 DAAKAM AFRKREELGSSVSVELMSVYLYVMYKGLKKDQWGPITNTR 98  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 850 DWSNKKVLPSPKNNVQKAVN\*ASPKKNGCTDVNSVYCTLSG \* \* \* \* \* 899  
 99 TGGVYAAHYRTLLKSLTPEMKEVTPPEV\*TDVRELVACETTKPVVYE 157  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 900 EYSLTEKNIELVSSSSMNGTCTVDGINSYSCITANFGKQNVN 948  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 158 GGGVNSRDLGNISGLSK \* \* \* \* \* TLEETVPVSGGRK \* \* \* \* \* PVLTSP 199  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 949 NVALGVGRTEVYKAGGRKAVVRYTGHESLQNGTGNKNGSCVGT 1004  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 200 ANHLSRQMSKIDVYGVHSLDPSI \* \* \* \* \* FATTLPQ \* \* \* \* \* 242  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 1004 SNTVSNGLTGYEGTFAVGVSGTVVANSLLAVSDLTNGTCHDSTAHRSVCAVP 1064  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 244 GAAKTCPL NYVNNYMC \* \* \* \* \* RLAAQDFEYSNVD \* \* \* \* \* 266  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 1064 TGGVTDLDDEVASVGRKAVNDELINSYCTVADYEGATGLDKDEYASSPKNGGT 1124  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 267 TSTNRRHGV \* \* \* \* \* GNKLLDGLGV \* \* \* \* \* NGKLRSSGTHKMLDQSGV \* \* \* \* \* 314  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 1124 CTDRINSYSLATLBNVTEINDECHTNCINRNVLTDTGG \* \* \* \* \* SGQCSGY 1177  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 915 GA NKLPSNCAKGR \* \* \* \* \* DENLGVGR \* \* \* \* \* TGRNPDP 351  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 1178 EDRGVGVAVNGLSNVSSSLATLGKSNVGVVGMADYIGSRGLKSGDINRIND 1247  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 952 GFAVGVTEVYCTLEKRRTHGV \* \* \* \* \* YRPAVAKKLPDVELESEE \* \* \* \* \* V 431  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 14 1238 G TCHNSGD TGVK CGLTWYCKKFNYSYMSANRHYHEAVQSGT 1286  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 97 402 GGVGVSYW 409

11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 DB 1287 GTFENRY 1294  
 RESULT 13  
 557956  
 ovine vascular endothelial growth factor - sheep  
 C/Spectrum: ovine endothelial atros, ovine adipon atros (domestic sheep)  
 C/Date: 13 Jan 1996 #sequence\_revision 03 Mar 1996 #tox\_change 03 Mar 1999  
 C/Accession: S57956  
 R. Bodmer, D.A.; Dalt, Y.; Li, J.; Jones, S.C.; Moor, R.M.  
 submitted to the EMBL Data Library, July 1995  
 A/Reference number: S57956  
 A/Accession: S57956  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-146  
 A/Cross-References: EMBL:089506; NID:0899450; PDB:0AA61677.1; PDB:0899451  
 Query Match 7.48; Score 174.5; DB 2; Length 146;  
 Best Local Similarity 34.98; Prod. No. 60; 06;  
 Matches 37; Conservative 17; Mismatches 42; Indels 14; Gaps 4;  
 114 ELKSLDNEKRLGMPKRWLTWKEKGAALNTEKPPCVSVKGGGNN 172  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 DB 58 EVMKMDVYGVSGCPLELVVPLSGDQKPVLSFANHTS\*PCMSKIDVYGVHSTLR 96  
 174 SDAAGMNTSTGYLSKSLPELVVPLSGDQKPVLSFANHTS\*PCMSKIDVYGVHSTLR 216  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 DB 97 EE-----FNITMOLMRKTRQSHLQSMSPGLGNKGVDPKRRKARV 138  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 RESULT 14  
 A33787  
 vascular endothelial growth factor (version 1) - bovine  
 C/Spectrum: Bos primigenius taurus (cattle)  
 C/Date: 16 Mar 1990 #sequence\_revision 16 Mar 1990 #tox\_change 05 Nov 1999  
 C/Accession: A33787  
 R. Krieger, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; et  
 al.  
 Biochem. Biophys. Res. Commun. 145: 1198-1206, 1989  
 Article: Vascular endothelial growth factor: a new member of the platelet derived gro-  
 A/Reference number: A33787  
 A/Accession: A33787  
 A/Status: ECLISARY  
 A/Molecule type: mRNA  
 A/Residues: 1-120  
 A/Cross-References: GEM:03750; NID:0163810; PDB:AAA0805.1; PDB:0163811  
 C/Keywords: alternative splicing  
 Query Match 7.48; Score 172.5; DB 2; Length 120;  
 Best Local Similarity 33.98; Prod. No. 5; 96-06;  
 Matches 37; Conservative 17; Mismatches 42; Indels 14; Gaps 4;  
 114 ELKSLDNEKRLGMPKRWLTWKEKGAALNTEKPPCVSVKGGGNN 172  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 DB 12 EVMKMDVYGVSGCPLELVVPLSGDQKPVLSFANHTS\*PCMSKIDVYGVHSTLR 96  
 174 SDAAGMNTSTGYLSKSLPELVVPLSGDQKPVLSFANHTS\*PCMSKIDVYGVHSTLR 216  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 DB 71 EE-----FNITMOLMRKTRQSHLQSMSPGLGNKGVDPKRRKARV 112  
 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : : 11 : : : : :  
 RESULT 15  
 A49128  
 cell fate determining gene Notch2 protein - rat  
 C/Spectrum: Rattus norvegicus (Norway rat)  
 C/Date: 21 Jan 1994 #sequence\_revision 18 Nov 1994 #tox\_change 13 Aug 1999  
 C/Accession: A49128  
 R. McGlamery, G.; Roberts, V.J.; Lemke, G.  
 Development 116: 941-941, 1992  
 Article: Notch2: a second mammalian Notch gene.

A: Reference number: A49128; M01D:93202015

A: Accession: A49128

A: Status: preliminary; not compared with conceptual translation

A: Molecule type: mRNA

A: Residues: 1-2471; SW1.

A: Experimental source: Schwann cell

A: Note: Sequence extracted from MBL backbone (NCBI:127811)

C: Superfamily: undetermined ankyrin repeat proteins; ankyrin repeat homology; EGF homology

F: 264-285/Domain: EGF homology <EGX1>

F: 799-830/Domain: EGF homology <EGF1>

F: 877-909/Domain: EGF homology <EGX2>

F: 1029-1060/Domain: EGF homology <EGF>

F: 1067-1098/Domain: EGF homology <EGX3>

F: 1153-1184/Domain: EGF homology <EGF3>

F: 1191-1222/Domain: EGF homology <EGX4>

F: 1476-1508/Domain: ankyrin repeat homology <AN1>

F: 1509-1541/Domain: ankyrin repeat homology <AN2>

F: 1943-1975/Domain: ankyrin repeat homology <AN3>

F: 1976-2008/Domain: ankyrin repeat homology <AN4>

F: 2009-2041/Domain: ankyrin repeat homology <AN5>

Query Match 7.88; Score 170; 18 2; Length 2471;

Best Local Similarity 22.08; Pred. No. 0.00018;

Matches 115; Conservative 44; Mismatches 184; Indels 180; Gaps 44;

```

QY 51 FEKRIIEFLRSV-----SSVRL--MSVLYLVYMKMKQ-----LRKQ 89
DB 508 FSEMCFEEDINVLANPQWAGS-VKVNFESELEHGFVGKQYUHMNQLSEPCNKQ 962
QY 90 WQGLITNTRGD-SVFAAAYNTFIIKSTUNEMPKTQMPREVCITVCKEFGAINTFE 148
DB 663 TCSIVVNSYICTGAGHGVHLENNI-----DKCTESSDFNGSTVVDGINSFSLCPVGF 1017
QY 149 KPP-V-SVVPVST--GVNS--FRI-----QGMNITGVLSKTLFEITVPLDGPV 195
DB 1018 IGPETVHINFSNPELNSATVVDNITVETCPHGYTRKNGVTVNIQSPSPENKGT 1077
QY 196 TISFANHTSRCKSLD-VKQVHSI-----LRKSLPAT-LPQ-----QAANKT----- 239
DB 1078 CAQKKAHPTCTPQWQWATGIVLNSCKAALQKQVPEHLQHSQICINAGNTHQC 1137
QY 240 PTNYVNNYMKPCTAQGFIFYSNVEDST-----NSFHLVQ-----GNKELEDPTQ- 288
DB 1138 PLGTT-GSY--CFEQLHFGASNDGKATCTPFTGTYRGTVPYGVGVNCEVEVEEQN 1193
QY 289 -----CVCKGRLRHSQ-----GPH-----KELDR--DSQCQV 314
DB 1194 QPQGNCTCTDVLVNHFKSCPEPTQLLCEENIDCVAGAPHCINQGVDPRIQVSCPEL 1253
QY 315 -----CK--NLEINSGANKEH-----FNLCQVCKR-----TQPRNP 348
DB 1254 PGPATRRFTGDIINCLSNPQSHQSHLQCTLRKNYQCVCKSAFTQKRCETFLAVQYQKPC 1313
QY 349 LNPCKCA-----CEQ-----TENTQCELGKKR 372
DB 1314 INQICAAVSNVPPGFTQHPHESAFACQSSQVWKGRRGQVHTIASGHHCTCP----- 1469
QY 473 HHQIC--SVRRRCANLKH--CDPGLSPFEVGRGVPSYV 409
DB 1470 NHRPFESGASNP-----QHGGTCYRQRPYYSKQSPFW 1407

```

Search completed: February 20, 2002, 16:26:18  
Job time: 326 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 20, 2002, 16:20:41 : Search time 42.36 Seconds

(without alignments)

725,604 Million goal - 63463/560

Title: US-09-534-376A-11

Sequence: 1 MHLGFLSLASGLAALIP.....SPSVKRVVSWKPPHIN 415

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 5

Searched: 522463 seqs, 7497490 positions

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

A\_Genoseq\_1101.\*  
1: /SITUS8/seqdata/genoseq/genoseq/AA1988.DAT.\*  
2: /SITUS8/seqdata/genoseq/genoseq/AA1989.DAT.\*  
3: /SITUS8/seqdata/genoseq/genoseq/AA1990.DAT.\*  
4: /SITUS8/seqdata/genoseq/genoseq/AA1991.DAT.\*  
5: /SITUS8/seqdata/genoseq/genoseq/AA1992.DAT.\*  
6: /SITUS8/seqdata/genoseq/genoseq/AA1993.DAT.\*  
7: /SITUS8/seqdata/genoseq/genoseq/AA1994.DAT.\*  
8: /SITUS8/seqdata/genoseq/genoseq/AA1995.DAT.\*  
9: /SITUS8/seqdata/genoseq/genoseq/AA1996.DAT.\*  
10: /SITUS8/seqdata/genoseq/genoseq/AA1997.DAT.\*  
11: /SITUS8/seqdata/genoseq/genoseq/AA1998.DAT.\*  
12: /SITUS8/seqdata/genoseq/genoseq/AA1999.DAT.\*  
13: /SITUS8/seqdata/genoseq/genoseq/AA2000.DAT.\*  
14: /SITUS8/seqdata/genoseq/genoseq/AA2001.DAT.\*  
15: /SITUS8/seqdata/genoseq/genoseq/AA2002.DAT.\*  
16: /SITUS8/seqdata/genoseq/genoseq/AA2003.DAT.\*  
17: /SITUS8/seqdata/genoseq/genoseq/AA2004.DAT.\*  
18: /SITUS8/seqdata/genoseq/genoseq/AA2005.DAT.\*  
19: /SITUS8/seqdata/genoseq/genoseq/AA2006.DAT.\*  
20: /SITUS8/seqdata/genoseq/genoseq/AA2007.DAT.\*  
21: /SITUS8/seqdata/genoseq/genoseq/AA2008.DAT.\*  
22: /SITUS8/seqdata/genoseq/genoseq/AA2009.DAT.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2433	100.0	415	19	AAW75742
2	2428	99.8	415	18	AAW00943
3	2048	87.8	419	18	AAW17837
4	2048	87.8	419	18	AAW00932
5	2048	87.8	419	19	AAW75740
6	2048	87.8	419	20	AAW86203
7	2048	87.8	419	21	AAW10648
8	2048	87.8	419	21	AAW29048
9	2048	87.8	419	21	AAW70749
10	2048	87.8	419	21	AAW70992
11	2048	87.8	419	22	AAW37605

12	2039	87.4	419	18	AAW17833	Human vascular end
13	2038	87.4	419	20	AAW30518	Vascular endothel
14	2038	87.4	419	20	AAW22420	Full length human
15	2038	87.4	419	21	AAW97144	Vascular endothel
16	2038	87.4	419	22	AAW97570	Human VEGF-B prote
17	2037	87.3	419	19	AAW75751	Vascular endothel
18	2035	87.2	419	18	AAW11478	Human vascular end
19	1969	84.4	399	20	AAW86237	Human VEGF-e full
20	1783	76.4	350	20	AAW30519	A truncated vascular
21	1783	76.4	350	20	AAW22321	Truncated human VE
22	1783	76.4	350	21	AAW97145	Truncated vascular
23	1783	76.4	350	21	AAW97577	Human VEGF-2 prote
24	1779	76.2	350	16	AAW86236	Vascular endothel
25	1747.5	74.9	418	18	AAW00934	Chall F114 recepto
26	1747.5	74.9	418	19	AAW75743	Quail vascular end
27	1658	71.1	318	20	AAW08284	Human growth facto
28	1621	69.5	337	20	AAW86232	Human VEGF-2 full
29	1590	69.2	302	20	AAW86233	Human VEGF-e full
30	1569	67.3	297	20	AAW86234	Human VEGF-e full
31	1536	65.8	292	20	AAW86235	Human VEGF-e full
32	696	29.8	354	19	AAW49536	Human VEGF-e growt
33	696	29.8	354	19	AAW51241	Homo sapiens vascu
34	696	29.8	354	19	AAW44293	Human vascular end
35	696	29.8	354	21	AAW10649	Human VEGF-D prote
36	696	29.8	354	21	AAW29049	Human VEGF-D prote
37	696	29.8	354	21	AAW70750	Human prepro-vascu
38	696	29.8	354	21	AAW70983	Human vascular end
39	696	29.8	354	22	AAW97573	Human VEGF-D1 prot
40	696	29.8	354	22	AAW37606	Human VEGF-D1 prot
41	695.5	29.8	325	19	AAW53240	Homo sapiens vascu
42	695.5	29.8	325	22	AAW97572	Human VEGF-D1 prote
43	695.5	29.8	325	22	AAW97573	Human VEGF-D1 prote
44	689.5	29.6	358	19	AAW14992	Murine VEGF-B induc
45	689.5	29.6	358	19	AAW37622	Mus musculus vascu

#### ALIGNMENTS

RESULT 1  
ID: AAW75742 standard: Protein: 415 AA.  
AC: AAW75742:  
--  
14 (first entry)  
--  
Mouse vascular endothelial growth factor C protein.  
DE: F114: vascular endothelial growth factor C: vascular endothelial cells;  
KW: lymphatic endothelial cells; myelopoiesis; angiogenesis; inflammation;  
KW: lymphatic endothelial cells; myelopoiesis; angiogenesis; inflammation;  
XX: Mus sp.  
XX: OS: Mus musculus  
XX: PN: M09833917-A1.  
XX: PD: 06-AUG-1998.  
XX: PF: 02-FEB-1998: 98W0-MS01973.  
XX: PR: 05-FEB-1997: 9708-0795430.  
XX: PA: (LUDWIG) LUDWIG INST CANCER RES.  
XX: PA: (DYHE-) UNIV HELSINKI LICENSING LTD.  
XX: PI: Altalo K, Jonkov V;  
XX: P1: WPL, 1996 437470/37.  
XX: DB: N-PSDB: AAW52577.  
XX: FT: New isolated vascular endothelial growth factor polypeptides)  
XX: used to develop products for treating, e.g., cancers, inflammation,







[illegible]

## RESULT 6

IL AAW86203 standard; protein; 419 AA.

AA AAW86203;  
AC

15-FHH-1999 (first entry)

AA Human vascular endothelial growth factor (VEGF)-C sequence.  
DE

VEGF; VEGF-related protein; vascular endothelial growth factor

KW Secretary: Col

KW lower limit is  
KW would be 100

Hollo sárjiers.

[illegible]

XX  
XX  
P1) 05 = NOV - 1 4448

XX  
XX  
711-Alpha-1000  
(9866)-11507001

XX  
DE 25-0100-16XX  
XX  
GOVT - GOVT ATTORNEYXX  
D1  
Wobles D.

XX	1000-00000000
XX	1000-00000000

XX

Pr Subunits lack pa

XX :  
XXXX

XX  
COTTON, IN THE LATE EIGHTEENTH.

growth factor (VbGF)-C protein. The invention provides a method for the amino acid sequence of human VbGF-C protein.

N-terminal to the first cyst of the core sequence deleted. Host cells

transcribed with expression vectors containing nucleotide acids encoding the truncated VBP subunits are used to produce the

CC expressed from gene therapy vectors, have in vivo and in vitro angiogenic

activity and are used to stimulate angiogenesis, particularly coronary collateral vessel development in cases of 'cardiac ischaemia' to stimulate

endothelial cell growth and migration in vitro; to treat heart disease; to treat ischaemia (ie a cardiac coronary or chronic lower limb) or to treat ischaemia (ie a cardiac coronary or chronic lower limb).

- CC ischaemia; stroke and peripheral vascular disease); to promote healing wounds (of skin or intestines) and to increase vascular permeability

[illegible]

Query Match: 87.88; Score 2048; DB 20; Length 419;  
Host Local Similarity: 85.48; Score 1954; DB 7; Length 419

Matches 358; Conservat 28; Mismatches 29; Indels 4; Gaps

QY 1 MHLPFLSLA\*SLAAALPSPRPATVVAFFSRIQPSAEFFSGEVKAFEGKILPEQL 60

1



KM Human: receptor tyrosine kinase; RTK; Flt4; fms like tyrosine kinase 4;  
 KM VEGFR-C: vascular endothelial growth factor receptor-3; chromosome 3q35;  
 KM cytotlastic tumour imaging; anti-tumour therapy; treatment; diagnosis;  
 KM neoplastic diseases; lymphoma; carcinoma; breast; squamous cell; melanoma;  
 KM sarcoma; malignancy; VEGF-C; vascular endothelial growth factor C;  
 XX  
 OS Homo sapiens.  
 FH Key location/qualifiers  
 FT 1..31  
 FT Peptide /label= Signal peptide  
 FT 32..103 /label= N-terminal peptide  
 FT /note= "Cleavage of this peptide from partially processed  
 VEGF-C produces a fully processed mature form of VEGF-C  
 of 21-43 kD which has high affinity to VEGFR-2"  
 FT 104..227  
 FT Protein /label= Mature\_VEGF-C  
 FT 228..419 /label= C-terminal peptide  
 FT /note= "This portion of sequence contains  
 remnants of signal peptide and the C-terminal  
 cleavage of signal peptide and the C-terminal  
 peptide produces a partially processed form of VEGF-C of  
 about 29 kD which has high affinity to Flt4 (VEGFR-3)"  
 FT 113..213  
 FT Binding-site /note= "This and signal fms VEGFR receptor are  
 at position 156 is essential for VEGFR-2 binding and at  
 165 is essential for VEGFR-2 and VEGFR-3 binding"  
 FT 131..211  
 FT Region /note= "Important for VEGF-C activity"  
 PN W:200021569-A1.  
 PD 20-APR-2000.  
 PF 08-OCT-1999; 99WO-0523525.  
 PE 09-OCT-1998; 98US-0169074.  
 PR (LUDW-) LUDWIG INST CANCER RES.  
 PA (OYME-) UNIV HELSINKI LICENSING LTD OY.  
 XX  
 XX  
 PI Alitalo K, Kaipainen A, Valtola R, Jussila E.  
 XX W61: 2000-317656/27.  
 XX  
 XX Treating neoplastic diseases such as lymphoma, carcinoma, melanomas  
 PI and sarcomas, involves administering a compound capable of inhibiting  
 PT binding of ligand proteins to fms like tyrosine kinase 4 receptor -  
 XX  
 XX Example 15-17, page 140-142; 14pp; English.  
 PS  
 XX The patent discloses a method to treat neoplastic disease characterised  
 CC by expression of fms like tyrosine kinase 4 (Flt4) receptor (also  
 CC referred as vascular endothelial growth factor receptor-3, VEGFR-3) in  
 CC endothelial cells of blood vessels adjacent to malignant neoplasm. The  
 CC method involves administering a compound that inhibits binding of a  
 CC ligand to Flt4 thereby inhibiting Flt4 mediated proliferation of vascular  
 CC endothelial cells. The compound is useful for treating neoplastic disease  
 CC such as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas  
 CC and sarcomas. Flt4 receptor tyrosine kinase binding compounds can be used  
 CC for manufacturing medicine useful for diagnostic screening, imaging and  
 CC treatment of malignancies characterised by Flt4-expressing blood cells  
 CC The Flt4 gene maps to chromosomal region 3q35 and is expressed as 5.8 kb  
 CC and 4.5 kb mRNAs which differ in their 3' sequences and are  
 CC differentially expressed in HFL and DAMI cell lines. Flt4  
 CC belongs to a subfamily of class III receptor tyrosine kinases (RTKs).  
 CC It is used as a target for tumour imaging and anti-tumour therapy.  
 CC The present sequence is a human prepro-vascular endothelial growth  
 CC factor C (VEGF-C), a specific example of Flt4 binding compound.  
 XX  
 XX Sequence 419 AA:

Query Match 67 93; Score 2048; FR 21; Length 419;  
 best local similarity 85.44; Prot. No. 7,96-151;  
 Matches 358; Conservative 28; Mismatches 29; Indels 4; Gaps 1;  
 QY 1 MHLLCFSLAGSLAAALPSPREPATVAAPESGLSPSEAPPGSGVAKFEKLEFOL 60  
 LB 1 MHLLGTSVACSLAALIPPEPAADAATESGLSDSPADPAATAYASKDLDEQ 60  
 QY 61 PEVSVDPTMSVLYPPWKKWKQCGPKCGMO---GPTI NPTGDSVKAAMNTEFLK 116  
 LB 61 PEVSVDPTMSVLYPPWKKWKQCGPKCGMO---GPTI NPTGDSVKAAMNTEFLK 120  
 QY 117 STDNFQKPTGMPDPVCTIVKSPGSAATNFPKPPVSVVPPGCGNSPGLGWNISTGY 176  
 LB 122 SDNFWKTPGPPVCTIVKSPGSAATNFPKPPVSVVPPGCGNSPGLGWNISTGY 180  
 QY 177 LSKTLPETTVPLSGPKRVTTSFANHTSPCKMSKLVYKQVHSLIPRSFNAT PQLYAN 216  
 LB 181 LSKTLPETTVPLSGPKRVTTSFANHTSPCKMSKLVYKQVHSLIPRSFNAT PQLYAN 240  
 QY 237 KCTGTHYVWNNWYPTFAAGCTLYFVWVETNDEWVQSPRELEEDPQVWVWVW 296  
 LB 241 KCTGTHYVWNNWYPTFAAGCTLYFVWVETNDEWVQSPRELEEDPQVWVWVW 300  
 QY 297 TSSGPKKLVKESVGVVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVW 356  
 LB 301 TSSGPKKLVKESVGVVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVW 360  
 QY 352 PTFNTEGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 416  
 LB 361 PTFNTEGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 419  
 RESULT 10  
 AAY70982  
 ID AAY70982 standard; Protein: 419 AA.  
 AC AAY70982;  
 XX  
 XX 09-AUG-2000 (first entry)  
 DE Human vascular endothelial growth factor (VEGF)-C protein.  
 XX  
 XX Vascular endothelial growth factor-C; VEGF; human; re-endothelialisation;  
 KW vascular endothelial growth factor receptor; VEGFR; vascular trauma;  
 KW blood vessel; cardiovascular surgery; anti-restenosis agent; prevention;  
 KW restenosis; stenosis; percutaneous transluminal coronary angioplasty.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key location/qualifiers  
 FT 1..31  
 FT Peptide /label= Signal peptide  
 FT /note= "Cleavage results in partially processed VEGF-C  
 protein (29 kD)"  
 FT 32..103  
 FT Peptide /label= Amino-terminal peptide  
 FT /note= "Cleavage produces a fully processed mature  
 VEGF-C protein (21-23 kD)"  
 FT 104..227  
 FT Protein /label= Mature\_human\_VEGF-C  
 FT /note= "Processed vascular epithelial growth factor-C"  
 FT 228..419  
 FT Binding-site /note= "Essential for VEGFR-2 and VEGFR-3 binding"  
 FT 131..211  
 FT Active-site /note= "Essential for biological activity of protein"  
 FT Binding-site 137  
 FT Binding-site /note= "Essential for VEGFR-2 and VEGFR-3 binding"  
 FT 156  
 FT Binding-site /note= "Essential for VEGFR-2 binding"  
 FT 165







XX	10	MAV	1999	9906	035050.21	
XX	11	MAE	1999	9805	0042105	
XX	12	MIN	1998	9805	0107997	
XX	13	(HUMA ) HUMAN	GENOME	SCI	1N1	
XX	14	W01	1999	991009/416		
XX	15	N	ESD	AA2105.23		
XX	16	New human vascular endothelial growth factor-2, used for treating, e.g., immune disorders and cancers				
XX	17	claim 12, fig 1A-E; 22pp; English				
XX	18	The present sequence represents vascular endothelial growth factor-2 (VEGF-2). The VEGF-2 polypeptides have activities similar to VEGF. The VEGF-2 polypeptides stimulate the growth of vascular endothelial cells, stimulate endothelial cell migration, stimulate angiogenesis, decrease blood pressure, and increase blood flow. The polypeptides and polypeptide can be used for preventing, treating or ameliorating a medical condition. The VEGF-2 polypeptides or polypeptides may be used in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or modulation (chemokines) of immune cells. The activity of these immune deficiencies or disorders may be detected, treated, such as cancer or autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or infectious. Examples of immunologic deficiency syndromes include blood production disorders, ataxia telangiectasia, common variable immunodeficiency, DiGeorge syndrome, HIV infection, HTLV-III infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocytic bactericidal dysfunction, severe combined immunodeficiency (SCID), Muckle-Wells disease, anemia, thrombocytopenia, or hemophilia. They can also be used to modulate enzymatic or thrombolytic activity. Similarly, allergic reactions and conditions such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated.				
XX	19	Sequence	419	AA		
XX	20	Genbank Match	87.4%	Score	20.68	108.20
XX	21	Genbank Match	85.0%	Score	No. 4,76-150	
XX	22	Match	456	Conservation	29	Mismatches 309
XX	23	Indels	4	Gaps		
XX	24	1	MLLGLPLSLALSLALAL	1	PSPEKFAVVAVFESSTGSEAFKPEKLEKLE	60
XX	25	1	1	1	1	1
XX	26	1	1	1	1	1
XX	27	1	1	1	1	1
XX	28	1	1	1	1	1
XX	29	1	1	1	1	1
XX	30	1	1	1	1	1
XX	31	1	1	1	1	1
XX	32	1	1	1	1	1
XX	33	1	1	1	1	1
XX	34	1	1	1	1	1
XX	35	1	1	1	1	1
XX	36	1	1	1	1	1
XX	37	1	1	1	1	1
XX	38	1	1	1	1	1
XX	39	1	1	1	1	1
XX	40	1	1	1	1	1
XX	41	1	1	1	1	1
XX	42	1	1	1	1	1
XX	43	1	1	1	1	1
XX	44	1	1	1	1	1
XX	45	1	1	1	1	1
XX	46	1	1	1	1	1
XX	47	1	1	1	1	1
XX	48	1	1	1	1	1
XX	49	1	1	1	1	1
XX	50	1	1	1	1	1
XX	51	1	1	1	1	1
XX	52	1	1	1	1	1
XX	53	1	1	1	1	1
XX	54	1	1	1	1	1
XX	55	1	1	1	1	1
XX	56	1	1	1	1	1
XX	57	1	1	1	1	1
XX	58	1	1	1	1	1
XX	59	1	1	1	1	1
XX	60	1	1	1	1	1
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XX	62	1	1	1	1	1
XX	63	1	1	1	1	1
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XX	73	1	1	1	1	1
XX	74	1	1	1	1	1
XX	75	1	1	1	1	1
XX	76	1	1	1	1	1
XX	77	1	1	1	1	1
XX	78	1	1	1	1	1
XX	79	1	1	1	1	1
XX	80	1	1	1	1	1
XX	81	1	1	1	1	1
XX	82	1	1	1	1	1
XX	83	1	1	1	1	1
XX	84	1	1	1	1	1

[illegible]



